STIC-Biotech/ChemLib

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From:	
Sent: To:	1
Subject:	$-\!$
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Mehta, Ashwin Monday, April 28, 2003 3:57 PM STIC-Biotech/ChemLib sequence search

STIC.

Please search the commercial and interference databases for the nucleotide sequences of SEQ ID NOs: 5 and 6 from 09/810,764.

My mail room is 9E12, office 9E07, art unit 1638.

Thank you, Ashwin Mehta

Ashwin Mehta United States Patent and Trademark Office Biotechnology Patent Examiner 703-306-4540 Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534

Online time:_

TYPE OF SEARCH:

NA Sequences:_____

AA Sequences:_____

Structures:_____

Bibliographic:_____

Litigation:_____

Full text:____

Patent Family:_____

Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_
Questel/Orbit:____
DRLink:____
Lexis/Nexis:____
Sequence Sys.:_
WWW/Internet:____
Other (specify):______

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein April 29, 2003, 09:33:59; Search time 75 Seconds (without alignments) 33.757 Million cell updates/sec Run on:

US-09-810-764A-5 90

1 RGKFERTKPGVNIGTIXXV 19 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Zea mays protein f	The same of the sa	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	C glutamicum prote	E. coli proliferat	. E. coli cellular p	E. coli cellular p	Haemophilus influe
SE			:										
SUMMARIES		ID	AAG40781		AAG18102	AAG52762	AAG18101	AAG52761	AAG93183	AAB15890	AAU34769	AAU34838	AAU35466
		OB	21	i	21	21	21	21	22	21	22	22	22
		Query Match Length DB 1	465		476	476	497	497	396	394	394	394	394
	ф	Query Match	86.7		80.0	80.0	80.0	80.0	7.97	73.3	73.3	73.3	73.3
		Score	78		72	72	72	72	69	99	99	99	99
		Result No.		•	2	٣	4	S	9	7	80	6	10

99US-0129845 99US-0130077

16-APR-1999; 19-APR-1999;

Haemophilus influe Salmonella typhi c Sequence of transl Sequence of transl Sequence of transl Sequence of elfamy	of of ruct bact	N-terminal sequenc Helicobacter pylor Helicobacter pylor Helicobacter pylor Pseudomonas aerugi Pseudomonas aerugi	teria mor ngation i eptococcu eptococcu eptococcu sophila m	Zea mays protein t Zea mays protein f Zea mays protein f Zea mays protein f Zea mays protein f Candida albicans e Chlamydia pneumoni C. pneumoniae CT32 C. trachomatis CT3 Chlamydia pneumoni
AAU35476 AAU38371 AAR20242 AAR20243 AAR20245	44710	AAW33404 AAW73036 AAW73035 AAU35822 AAU36402 AAU36409	ABB48242 AAW30303 AAW37578 ABP30281 ABP25922 ABP25923 ABB62027	AAG12252 AAG12476 AAG12474 AAG44634 AAG44633 AAB03444 AAY34672 AAU38889 AAU38909
22 22 13 13	223333	755 755 755 755 755 755 755 755 755 755	22 23 23 23 23 23 23 23 23	21 22 22 23 23
394 396 396 396	3906 396 132 436	3 2 2 2 2 2 2 3 3 9 9 9 9 9 9 9 9 9 9 9	3995 3998 3998 404 415	86 111 129 150 175 426 394 394 394
m m 01 01 01 0	1000000	~ ~ ~ ~ ~ ~ ~ ~ ~ ~	663.3 63.3 63.3 64.2 64.2 65.2	61.1 61.1 61.1 61.1 61.1 58.9 58.9
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ALIGNMENTS

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                         Zea mays protein fragment SEQ ID NO: 50648.
                 AAG40781 standard; Protein; 465 AA.
                                                                                                                                                                                                                 99US-0121825.
99US-0123180.
99US-0123548.
                                                                                                                                                                                              2000EP-0301439
                                                                                                                                                                                                                                              99US-0125788
99US-0126264
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99US-0128714
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                                                        (first entry)
                                                                                                                                     Zea mays subsp. mays.
                                                                                                                                                        EP1033405-A2.
                                                                                                                                                                                                                 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                              25-FEB-2000;
                                                        18-OCT-2000
                                                                                                                                                                                                                                                                                     06-APR-1999;
08-APR-1999;
                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                23-MAR-1999;
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                                                                                                                                                                                                                                                                  29-MAR-1999;
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                                     AAG40781;
RESULT 1
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1444 1444	28 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
99US-0130449. 99US-01310489. 99US-01310510. 99US-0131048. 99US-0131489. 99US-0132486. 99US-0132486. 99US-0132487. 99US-0132487. 99US-0134218. 99US-0134218. 99US-0134218. 99US-0134219. 99US-0134219. 99US-0134219. 99US-0134219. 99US-013124. 99US-013124. 99US-013124. 99US-013124. 99US-013124. 99US-013124. 99US-013124. 99US-013124. 99US-013452. 99US-013455. 99US-01345. 99US-01345. 99US-01345. 99US-01345. 99US-01345. 99US-01345.	990S-01420 990S-01420 990S-01428 990S-01429 990S-01429 990S-01435 990S-01440 990S-01440 990S-01443 990S-01443
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990S-0135529-
990S-0135529-
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990S-0142977
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990S-014400S
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99US-0145088.
99US-0145085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                 Length 465;
                                                                                                                                                                                                                                                                                                                              Score 78; DB 21; Length 40. Pred. No. 5.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 19377.
                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG18102 standard; Protein; 476 AA
 990S - 0159331 . 990S - 0159331 . 990S - 0159534 . 990S - 0159584 . 990S - 0160741 . 990S - 0160768 . 990S - 0160980 . 990S - 0161359 . 990S - 0161359 . 990S - 0161350 . 990S - 0161920 . 990S - 0161920 . 990S - 0161993
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990S-0123180.
990S-0125788.
990S-012578.
990S-0126785.
                                                                                                                                                                                                                                                                                                                                              86.7%;
84.2%;
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990S-0128714
990S-0128845
990S-0130077,
990S-0130891,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0131449.
99US-0132048.
99US-0132407.
99US-0132484.
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                                                                                                                                                                                                                                                                                                                99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
14 - OCT - 1999;
14 - OCT - 1999;
18 - OCT - 1999;
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21 - OCT - 1999;
22 - OCT - 1999;
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25 - OCT - 1999;
26 - OCT - 1999;
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28 - OCT - 1999;
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23-MAR-1999;
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29-MAR-1999;
20-APR-1999;
06-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG18102;
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                                                                                                                                                                                                                                                                                                                                                                        Matches
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AAG18102
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-OCT-1999;
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                                                                                                                                                            Gaps
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0
                                                                                                                                           Score 72; DB 21; Length 476; Pred. No. 0.00059;
                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 67107.
                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                      AAG52762 standard; Protein; 476 AA.
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990S-0123548
990S-0125788.
990S-0126264.
990S-0126785.
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99US-0130510.
99US-0130891.
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990S-0132048
990S-0132480
990S-0132486
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990S-0134286
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990S-0134286
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99US-0129845.
99US-0130077.
99US-0160770.
99US-0160814.
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99US-0161405.
99US-0161405.
99US-0161350.
99US-0161360.
99US-0161360.
99US-0161361.
                                                                                                                                              80.0%;
78.9%;
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                                                                                                                                                                             RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                     70 RGKFERKKPHVNIGTIGHV 88
                                                                                                                                                                                                                                                                       18-OCT-2000 (first entry)
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                        EP1033405-A2
                                                                                                                                             Query Match
Best Local Simil
Matches 15;
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14-MAY-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                       AAG52762;
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   Qγ
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990x - 0145913 990x - 0145918 990x - 0145919 990x - 0145386 990x - 0146386 990x - 0146389 990x - 0147302 990x - 0147303 990x - 0149313 990x - 0149313 990x - 0149313 990x - 0149313 990x - 0149313 990x - 0150884 990x - 0149313 990x - 015086 990x - 0160814 990x - 0160816 990x - 016088
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21-JUN-1999;
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                                                                           Score 72; DB 21;
Pred. No. 0.00059;
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78.9%;
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                                                                                            Conservative
                                                                                                                                                                                                                                                           Arabidopsis thaliana
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13-0CT-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                   Length 497;
                                                          4; Indels
                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 67106.
                                Score 72; DB 21;
Pred. No. 0.00062;
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                                 Query Match 80.0%;
Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                           91 RGKFERKKPHVNIGTIGHV 109
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990S-0136392.
990S-0136782.
990S-013722.
990S-0137528.
99US-0161993
99US-0162142
                                                                               1 RGKFERTKPGVNIGTIXXV 19
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28-OCT-1999;
29-OCT-1999;
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06-MAY-1999;
07-MAY-1999;
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Escherichia coli,
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AAU34769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, massuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                       mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                    Hayashi M, Ochiai K, Yokol H;
                                                                                                                                                     Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .<u>`</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 29; SEQ ID NO: 6937; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.7%; Score 69; DB 22; Length 396; 73.7%; Pred. No. 0.0016; Live 1; Mismatches 4; Indels
                                                                                                                                 C glutamicum protein fragment SEQ ID NO: 6937.
                                                                                                                                                                                                                                                                                                                        Mizoguchi H, Ando S, Hayash
Tkeda M, Ozaki A;
                                                                     AAG93183 standard; Protein; 396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB15890 standard; Protein; 394 AA.
             91 RGKFERKKPHVNIGTIGHV 109
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1 RGKFERTKPGVNIGTIXXV 19
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03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                    Corynebacterium glutamicum.
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                                                                                                                                                                organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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Tateishi N,
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AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65809 to AAA66055 and AAB15806 to AAA65809 to AAA66055 and AAB15806 to AAA65090 to AAA66055 and AAB15806 to AAA6605 and Proliferation inhibiting nucleotide inserts in an example from the present invention. Methods from the present invention can be used to identify a proliferation. This proliferation inhibiting an example from the present invention. Methods from the present invention and be used to identify a proliferation-required gene in a microorganism, by contacting an microorganism with a proliferation-required gene activity inhibitory nucleic acid identified in another organism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can be used for antisense therapy for killing bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                       antimicrobial; bacterial growth; antisense therapy; antibacterial.
                                                                                                                      E. coli proliferation associated protein sequence SEQ ID NO:247.
                                                                                                                                                                                       Escherichia coli; E. coli; proliferation; inhibition; screening
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                                                           05-OCT-2000 (first entry)
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AAB15890
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Haemophilus influenzae.
             WO200170955-A2.
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                                           27-SEP-2001.
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Consential prokaryotic cellular proliferation protein.

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Yamamoto RT, Xu HH;
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Pred. No. 0.0052;
1; Mismatches 3; Indels
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76.5%;
                                                                                                                                2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                  21-MAR-2001; 2001WO-US09180.
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mes 13; Conservative
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                     WO200170955-A2.
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22-DEC-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential comes, their use in the discovery of novel antibiotics, the essential comes, their use in the discovery of novel antibiotics, the essential comes, themselves and the encoded proteins. The prokaryotes used are pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen correction suclets acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Contact the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotics, comprise sequences of antisense nucleic acids
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                                                                                             23-MAY-2000; 20000S-206848P.
26-MAY-2000; 2000US-207727P.
23-CCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-253931P.
16-FEB-2001; 2001US-269308P.
21-MAR-2001; 2001WO-US09180.
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Best Local Similarity 76.55
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                                                                                                                                                                                                                                                                                Ohlsen KL, Zyskind JW, Wall D,
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200005-20727P.
200005-242578P.
200005-253625P.
200105-267931P.
                                                                                21-MAR-2001; 2001WO-US09180
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nes 13; Conservative
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                                                                                                                                                                                                                                                                                               Xu HH;
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                 WO200170955-A2.
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                                                                                                                                 23-MAY-2000;
26-MAY-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruqinosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
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2000US-207727P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-611495/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS53335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi.
WO200170955-A2.
                                                                                                                                                                                                                                                                                                   23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /amamoto RT,
                                                                                                                                                                                                                                                                          26-MAY-2000;
                                                                                                                                                                                                           21-MAR-2000;
                                                                                                                                                                                                                                              23-MAY-2000;
                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sednence
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WPI; 1992-017874/03.
N-PSDB; AAQ20216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      )2-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luiten RGM,
Woudt LP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-1990;
                                                        02-JUL-1991;
                                                                               02-JUL-1991;
10-JUL-1990;
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                                 15-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP466251-A.
         EP466251-A.
                                                                                                                                                                                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR20243;
                                                                                                                                                      Woudt LP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aucus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faccilis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention antibodies capable of binding to the expresse proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen corrections in the sequence data for this patent for the required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Con the printed specification, but was obtained in electronic form part contains the printed specification, but was obtained in electronic contains the printed probablished_pct_sequences.
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                                                                                                                                                                                                    Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of translation elongation factor Tul encoded by tufl gene.
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                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                    Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%; Score 66; DB 22; Length 409; 76.5%; Pred. No. 0.0054; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elfamycin resistant actinomycetes; antibiotic resistant; elongation factor.
                                                                                                                                                                                                   Haselbeck R, Ohlsen KL, Zyskind JW, Wall D,
Yamamoto RT, Xu HH;
                                                                                                                                                                                                                                                                                                           Example 3; Seq ID No 13964; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR20242 standard; Protein; 396 AA.
                                                                                          23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-CCT-2000; 2000US-242578P.
27-NOY-2000; 2000US-25525P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
                                                           21-MAR-2001; 2001WO-US09180.
                                                                                  2000US-191078P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-APR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces ramocissimus
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                                                                                                                                                                                                                                        WPI; 2001-611495/70.
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 AA;
                                                                                                                                                                                                                                                  N-PSDB; AAS56230
            WO200170955-A2
                                                                                  21-MAR-2000;
                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of translation elongation factor Tu2 encoded by tuf2 gene.
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                                                                                                                                                                                        Luiten RGM, Kerkman R, Bosch L, Vijgenboom E, Heinstra PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65; DB 13; Length 396; Pred. No. 0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                         used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elfamycin resistant actinomycetes; antibiotic resistant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kerkman R, Bosch L, Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                         New protein conferring resistance to elfamycin -
                                                                                                                                                                                                                                                                                                                                                                                      transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Fig 1 and Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR20243 standard; Protein; 396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.2%;
63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91EP-0201702.
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91EP-0201702.
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                                                   91EP-0201702
                                                                             90EP-0201851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces ramocissimus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.2'
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KONN ) GIST-BROCADES NV.
                                                                                                                                    (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                        WPI; 1992-017874/03.
N-PSDB; AAQ20215.
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Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistrant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. Of elfamycin by actinomycetes is removed by mutating the gene tuf into tufR encoding a protein, resistant to the elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                New protein conferring resistance to elfamycin - used to
                                       transform streptomycetes to resistant phenotype
                                                                                      Example; Pages 16-18; 35pp; English.
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Query Match 72.2%; Score 65; DB 13; Length 396; Best Local Similarity 63.2%; Pred. No. 0.0077; Matches 12; Conservative 3; Mismatches 4; Indels 1 RGKFERTKPGVNIGTIXXV 19

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Sequence 396 AA;

2 KAKFQRTKPHVNIGTIGHI 20

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Gaps

0

AAR20245 standard; Protein; 396 AA.

15-APR-1992 (first entry)

Sequence of elfamycin-resistant elingation factor EF-TuR Val 378 encoded by SrtufRl gene. Elfamycin resistant actinomycetes; antibiotic resistant; elongation factor.

Streptomyces ramocissimus.

15-JAN-1992. EP466251-A.

91EP-0201702. 02-JUL-1991;

91EP-0201702 90EP-0201851 02-JUL-1991; 10-JUL-1990;

(KONN) GIST-BROCADES NV.

Luiten RGM, Kerkman R, Bosch L, Vijgenboom E, Heinstra PW;

Woudt LP;

WPI; 1992-017874/03. N-PSDB; AAQ20218 New protein conferring resistance to elfamycin - used to transform streptomycetes to resistant pheno-type

Claim 6; Pages 13-15; 35pp; English.

Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. Of elfamycin by actinomycetes is removed by mutating the gene tuf into tuff encoding a protein resistant to elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.

396 AA; Sequence

Gaps ö Score 65; DB 13; Length 396; Pred. No. 0.0077; 4; Indels Mismatches 3; Query Match 72.2%; Best Local Similarity 63.2%; Matches 12; Conservative

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1 RGKFERTKPGVNIGTIXXV 19 δ

: ||||||| ||:||| : 2 KAKFERTKPHVNMGTIGHI 20 a

Search completed: April 29, 2003, 09:40:23 Job time : 77 secs

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GenCore version 5.1.4_-p5_-4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

(without alignments) 42.478 Million cell updates/sec April 29, 2003, 09:38:19 ; Search time 43 Seconds

1 RGKFERTKPGVNIGTIXXV 19 US-09-810-764A-5 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* PIR_73:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

translation elonga protein translatio translation elonga translation elonga elongation factor translation elonga elongation factor translation elonga protein translatio translation elonga elongation Factor Description SUMMARIES J02240 S36183 G87143 E75533 536184 AH3344 S31151 r06821 523908 PC4060 Query Match Length DB Kesult ٠ ک

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EFECT BTECTA S13561 S13560 E64078 F91152 G82337 G82337 AB0658 AB0657 AE0025 AB0934 AD1005 A44795	
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

ALIGNMENTS

-	
2	663
3	9

translation elongation factor EF-Tu - Pseudomonas cepacia

C;Species: Pseudomonas cepacia C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 02-Feb-2001 C; Accession: D60663

R;Ludwig, W.; Walzenegger, M.; Betzl, D.; Leidel, E.; Lenz, T.; Ludvigsen, A.; Moell Arch. Microbiol. 153, 241-247, 1990
A;Title: Complete nucleotide sequences of seven eubacterial genes coding for the elo A;Reference number: A60663; WUID:90240875; PMID:2110445

A.Status: not compared with conceptual translation
A.Status: not compared with conceptual translation
A.Nolecule type: DNA
A.Residues: 1.396 - CLUD>
A.Residues: 1.396 - CLUD>
A.Residues: 1.396 - CLUD>
C.Residues: 1.396 - CLUD - CLUD
C.Residues: 1.396 - CLUD - CLUD
C.Residues: 1.396 -

ö Gaps ó; 82.2%; Score 74; DB 2; Length 396; 73.7%; Pred. No. 9.3e-05; Live 2; Mismatches 3; Indels Local Similarity 73.79 hes 14; Conservative Query Match Matches

1 RGKFERTKPGVNIGTIXXV 19 δ

3 KGKFERTKPHVNVGTIGHV 21 g

translation elongation factor EF-Tu [imported] - Nostoc sp. (strain PCC 7120)

C; Species: Nostoc sp.
A; Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: AB2348
B; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigo Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabate A; Itle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUD:21595285; PMID:11759840

A; Status: preliminary

A;Molecule type: DNA A;Residues: 1-409 <KURX> A;Cross-references: GB:BA000019; PIDN:BAB76036.1; PID:g17133473; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:

A,Gene: tufA C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom

translation elonga

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C;Keywords: chloroplast; GTP binding; nucleotide binding; P-loop; protein biosynthesi F;1-69/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;70-478/Product: translation elongation factor Tu #status predicted <MAT>
F;82-208/Domain: translation elongation factor Tu homology <ETU>
F;88-208/Fregion: uncleotide-binding motif A (P-loop)
F;205-208/Region: GTP-binding NKXD motif F;443-445/Region: GTP-binding SAK/L motif F;443-445/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation elongation factor EF-Tu.A precursor, chloroplast - wood tobacco (5) Epecies. Nicotiana sylvestris (wood tobacco)
C; Species. Nicotiana sylvestris (wood tobacco)
C; Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 02-Feb-2001
C; Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 02-Feb-2001
C; Accession: S36183; S37674, 1993
A; Mittle: Purification of chloroplast elongation factor Tu and cDNA analysis in tobacc A; Title: Purification of chloroplast elongation factor Tu and cDNA analysis in tobacc A; Title: Purification of chloroplast elongation factor Tu and cDNA analysis in tobacc A; Title: Purification of chloroplast elongation factor Tu and cDNA analysis in tobacc A; Title: Purification of chloroplast elongation factor Tu and cDNA analysis in tobacc A; Testences: GB:D11375
A; Residues: 1-478 eAURIA
A; Residues: 1-478 eAURIA
A; Reference number: S37674
A; Molecule type: mRNA
A; Residues: 1-457 cAURIZ
A; Cooss-references: GB:D11375; NID:g218309; PIDN:BAA01974.1; PID:g218310
A; Cross-references: GB:D11375; NID:g218309; PIDN:BAA01974.1; PID:g218310
A; Cross-references: GB:D11375; NID:g218309; PIDN:BAA01974.1; PID:g218310
A; Residues: 1-457 cAURIZ
A; Residues: 1-458 cAURIZ
A; Residues: 1-478 cAURIZ
A; Residues: 1-478 cAURIZ
A; Residues: 1-
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A; Reference number: S40614; MUID:94373864; PMID:8087886
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C: Superfamily: translation elongation factor Tu; translation elongation factor Tu hc
C: Superfamily: translation elongation nucleotide binding; P-loop; protein biosynthes
C: Keywords: chloroplast; GTP binding; nucleotide binding; P-loop; protein biosynthes
C: Keywords: chloroplast; B-status predicted <TWP>
F:1-70/Domain: translation elongation factor Tu.A *status predicted <MAT>
F:32-208/Domain: translation elongation factor Tu homology <FTU>
F:88-95/Region: nucleotide-binding the MCD motif A (P-loop)
F:305-208/Region: GTP-binding NKXD motif
F:343-345/Region: GTP-binding SAK/L motif
F:34,95,131,205,206,208,243/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser)
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A; Cross-references: EMBL:D11469; NID:g459238; PIDN:BAA02027.1; PID:g459239
R; Sugita, M; Murayama, Y; Sugiura, M.
Curr. Genet. 25, 164-168, 1994
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78.9%; Pred. No. 0.00025;
iive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%; Score 72; DB 2; 78.9%; Pred. No. 0.00025;
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A;Residues: 1-111 <SUG2>
Cross-references: EMBL:D11469
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGKFERTKPGVNIGTIXXV 19
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Matches 15; Conserv
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Cramslation elongation factor EF-Tu precursor - common tobacco
Cracesion: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Feb-2001
Cracesion: J02240
Cracesion: J02240
A; Title: Cloning and nucleotide sequence of a tobacco chloroplast translational elongati
A; Title: Cloning and nucleotide sequence of a tobacco chloroplast translational elongati
A; Article: J02240
A; Molecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-478 cURS
C; Comment: This protein is an essential component for protein synthesis that functions by Genetics:
C; Genetics:
C; Genetics:
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homoloc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Genome: nuclear

A Genome: nuclear

C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
C; Superfamily: translation elongation; nucleotide binding; P-loop; protein biosynthesis
C; Reywords: chloroplast; GTP binding; nucleotide binding; P-loop; protein biosynthesis
F; Re 4.74 Product: translation elongation factor Tu #status predicted <MAT>
F; Re 4.74 Product: translation elongation factor Tu homology <ETU>
F; Re 0.39 Region: nucleotide-binding motif A (P-loop)
F; Re 0.39 Region: GTP-binding SAK/L motif
F; 241-243 Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #st
F; 92, 93, 129, 203, 204, 206, 241/Binding site: Mg-GTP (Lys, Thr, Thr, Thr, Asn, Lys, Asp, Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X52256; NID:g22564; PIDN:CAA36498.1; PID:g22565
A;Cross-references: EMBL:X52256; NID:g22565; B.W.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke submitted to the Protein Sequence Database, June 1999
A*Reference number: 216991
A*Accession: T10578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation elongation factor EF-Tu precursor, chloroplast - Arabidopsis thaliana N.Alternate names: protein F9F13.10
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 02-Feb-2001
C.Species: 30-Sep-1951 #sequence_revision 30-Sep-1991 #text_change 02-Feb-2001
C.Species: 30-Sep-1991 30-Sep-1991 #text_change 02-Feb-2001
C.Specie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Residues: 15-476 <BEV>
A;Residues: 15-476 <BEV>
A;Cross-references: EMBL:AL080253; GSPDB:GN00062; ATSP:F9F13.10
A;Experimental source: cultivar Columbia; BAC clone F9F13
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 2; Length 476; Pred. No. 0.00025;
                                                                                                                         Length 409;
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                                                                                                                                   80.0%; Score 72; DB 2; I
78.9%; Pred. No. 0.00021;
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                             Query Match 80.09
Best Local Similarity 78.99
Matches 15; Conservative
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es 15; Conserva
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translation elongation factor EF-Tu.B precursor, chloroplast - wood tobacco C;Species: Nicotiana sylvestris (wood tobacco)
C;Species: Nicotiana sylvestris (wood tobacco)
C;Accession: S56184, S37675; S46549; S40615
R;Murayama, Y.; Matsubayashi, T.; Sugita, M.; Sugiura, M.
Plant Mol. Biol. 22, 767-774, 1993
A;Fille: Purification of chloroplast elongation factor Tu and cDNA analysis in tobacconsideration of chloroplast elongation; PMID:8358028
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A:Reference number: S40614; MUID:94373864; PMID:8087886
A:Accession: S40615
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F;78-485/Product: translation elongation factor Tu B #status predicted <MAT>
F;89-215/Domain: translation elongation factor Tu be momelogy <ETU>
F;99-102/Region: uncleotide-binding motif A (P-loop)
F;112-215/Region: GTP-binding NKXD motif
F;250-252/Region: GTP-binding SAK/L motif
F;101,102,138,212,213,215,250/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser
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R; Murayama, Y.; Matsubayashi, T.; Sugita, M.; Sugiura, M.
Plant Mol. Biol. 22, 767-774, 1993
A; Title: Purification of chloroplast elongation factor Tu and cDNA analysis in tobacc A; Reference number: S36183; MUID: 93363910; PMID: 8358028
A; Accession: S39153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R'Sugita, M.; Murayama, Y.; Sugiura, M.
submitted to the EMBL Data Library, June 1992
A; Description: Structure and differential expression of two distinct genes encoding
A; Reference number: S46548
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C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-430, TMS', 434-448,'NM', 451-482,'IL', 485 <SUG1>
A;Cross-references: EMBL:D11470; NID:g459240; PIDN:BAA02028.1; PID:g459241
R;Sugita, M.; Murayama, Y.; Sugiura, M.
Curr. Genet. 25, 164-168, 1994
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A;Residues: 61-430, 'IMS', 434-448,'NM', 451-482,'ILE' <MU2>
A;Cross-references: GB:D11376; NID:9218311; PIDN:BAA01975.1; PID:9218312
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Pred. No. 0.00025;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Murayama, Y.; Matsubayashi, T.; Sugita, M.; Sugiura, submitted to the EMBL Data Library, June 1992
A;Reference number: S37674
A;Accession: S37675
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78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-103 <SUG2>
                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-485 <MUR>
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C; Species: Glycine max (soybean)
C; Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 02-Feb-2001
C; Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 02-Feb-2001
C; Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 02-Feb-2001
C; Accession: S60659
R; Maurer, F; Murone, M.; Stutz, E.
Submitted to the EMBL Data Library, July 1995
A; Description: The nuclear genome of soybean contains four tuf genes belonging to two su A; Reterence number: S60659
A; Recreated number: S60659
A; Accession: S60659
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-479 <AMU>
A; Residues: 1-479 <AMU>
A; Residues: 1-479 <AMU>
A; Genetics:
C; Genetics:
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homology C; Reywords: chloroplast; GTP binding; nucleotide binding; P-loop; protein biosynthesis
C; Superfamily: translation elongation factor Tu homology <ETU>
F; 80-96, Region: nucleotide-binding mixib motif A (P-loop)
F; 200-209/Region: GTP-binding mixib motif
F; 206-209/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #st
                                                                                                                                                                                                                                                                        C; Accession: $21567
Shony. C; Stutz, E.
Submitted to the EMBL Data Library, May 1992
A; Description: Soybean (glycine max 1.) nuclear DNA: structure and expression of chlorop A; Reference number: $21567
A; Molecule type: DNA
A; Residues: 1-479 < BON>
A; Coss-references: EMBL: X66062; NID:918775; PIDN:CAA46864.1; PID:918776
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genes: tufA
A;Genes: tufA
A;Genome: chloroplast
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo
C;Supwords: chloroplast; GTP binding; nucleotide binding; P-loop; protein biosynthesis
F;83-209/Domain: translation elongation factor Tu homology <ETU>
F;89-96/Region: nucleotide-binding mixto motif A (P-loop)
F;206-209/Region: GTP-binding Nixto motif
F;244-246/Region: GTP-binding Six/L motif
F;95,96,132,206,207,209,244/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #st
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                                                                                                                                                                     translation elongation factor EF-Tu precursor - soybean chloroplast C;Species: chloroplast Glycine max (soybean) c;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Feb-2001 C;Accession: S21567
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72 RGKFERKKPHVNIGTIGHV
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les 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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S36184
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Score 70; DB 2; Length 18; Pred. No. 1.9e-05;

77.8%; 87.5%;

Best Local Similarity

Query Match

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protein translation elongation factor Tu (EF-tu) [imported] - Brucella melitensis (st C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                            R.Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov S. Delvecchio, V.G.; Kapatral, V.; Relkor, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
A;Accession: AE3346
A;Status: preliminary
A;Molecule type: DMA
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A;Map position: I
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
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C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 02-Feb-2001
C;Accession: C11672
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
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A;Residues: 1.394 - AND>
A;Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15101.1; PID:g386
A;Experimental source: strain Madrid E
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C.Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
C.Superfamily: translation elongation factor Tu homology <PTU>
C.S. Taranslation elongation factor Tu homology <PTU>
F;13-139/Domain: translation elongation factor Tu homology <PTU>
F;13-26/Region: nucleotide-binding motif A (P-loop)
F;135-139/Region: GTP-binding SAK/L motif
F;25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #
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A;Accession: C71672
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 02-Feb-2001
C;Accession: S62726; F82879
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73.7%; Pred. No. 0.00066;
:ive 1; Mismatches 4; Indels
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Matches 14; Conservative
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Matches 14; Conserv
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RRAD, VK.; Whitlock, J.A.; Progulske-Fox, A.
submitted to the EMBL Data Library, June 1992
A:Description: Cloning, characterization, and sequencing of two hemagglutinin genes from A:Description: Cloning, characterization, and sequencing of two hemagglutinin genes from A:Description: S23847
A:Accession: $2381
A:Molecule type: DNA
A:Residues: 1-46 <RAD>
A:Residues: 1-46 <RAD>
A:Experimental source: Eikenella corrodens ATCC 23834
C:Genetics:
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S.Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo
C;Kyworda: GTP binding; nucleotide binding; P-loop; protein biosynthesis
F;19-26/Region: nucleotide-binding motif A (P-loop)
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R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensi A;Reference number: S78238
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
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C;Species: chloroplast Odontella sinensis
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                               C;Species: Eikenélla corrodens
C;Date: 12-Feb-1993 #sequence_revision 08-Nov-1996 #text_change 02-Feb-2001
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78.9%; Pred. No. 0.00046;
Live 0; Mismatches 4;
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   Mismatches
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   14; Conservative
                                                                                              RGKFERTKPGVNIGTI 16
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Matches 15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S78248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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      Matches
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A;Status: preliminary
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A;Relass. DNA
A;Residues: 1:394 <RAB: 214275; NID:9498790; PIDN:CAA84029.1; PID:9498791
B;Glass, J.I; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
B;Glass, J.I; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
B;Glass, J.I; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
B;Glass, J.I; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
B;Glass, J.I; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
B;Glass, J.I; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
B;Reference number: A82870
A;Reference number: A82870
A;Respection: J.394 <GLA>
A;Respection: Glass, Glass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Rickettsia conorii
Ricketa, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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Pred. No. 0.00066;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
submitted to the EMBL Data Library, June 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.7%;
Best Local Similarity 73.7%;
Matches 14; Conservative
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                                        A; Reference number: $62726
A; Accession: $62726
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A;Molecule type: DNA
A;Residues: 1-394 <KUR>
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H97825
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Search completed: April 29, 2003, 09:42:20 Job time : 44 secs

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34 66 73.3 394 EFTB_PASMU ES7966 pasteurella 35 66 73.3 396 EFTU_MYCTU ES7966 pasteurella 36 65 73.3 418 EFTU_PORPU E71501 mycobacteri 39 64 71.1 397 EFTZ_STRRA E722 STRRA E722 STRCA 42 64 71.1 397 EFTU_AGRTU F724 E724 STRCA E724 E724 STRCA E7	PRTPLARIED DETTOLINE STANDARD; PRT; 391 AA. DETTOLINE STANDARD; PRTP, 30 AR. CONTROL OF CONTROL OF CONTROL OF AREA AND CONTROL OF A CON	
Copyright (c) 1993 - 2003 Compugen Ltd. Mun on: April 29, 2003, 09:36:24; Search time 25 Seconds Title: US-09-810-764A-5 Sequence: US-09-810-764A-5 Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5 Total	### Parameters: 112 #### #### ########################	66 73.3 393 1 BFTU_AREIN P02990 (66 73.3 394 1 BFTA_PASMU P21694 8 P57939 p57939 p57939 p

DR TIGRFAMS; TIGR00485; EF-TU: 1.

DR PROSITE; PS00301; EFACTOR_GTP; 1.

KW Elongation factor; Protein biosynthesis; GTP-binding;

2 08:51:22 2003 Fri May

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RESULT 3
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                                                                                                                                                                                                                              SEQUENCE FROM N.A. pubmed=2110445; Leidel E., Lenz T., Ludvigsen A., MEDLINE=90240875; Pubmed=2110445; K.H., Ludwig W., Weizenegger M., Schleifer K.H., Moellenböf E., Wenzig P., Schleifer K.H., Moellenböf E., Wenzig P., Schleifer Seven eubacterial genes coding for Moellenböf E., Wenzig P., Schleifer Seven eubacterial and phylogenetic the elongation factor Tu: functional, structural and phylogenetic
                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GIP-BINDING ELONGATION FACTOR FAMILY.
-ER-TU/FE-1A SUBFAMILY.
-- PIR: D60663: D60663.
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                                                                                                                                                                                                                                                                              Arch. Microbiol. 153:241-247(1990). THE GTP-DEPENDENT BINDING OF Arch. Wilcrobiol. THIS PROMEIS THE GTP-DEPENDENT BINDING -1- FUNCTION: THIS PROTEIN PROMOTES THEOSOMES DURING PROTEIN AMINOACYL. TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%; score 74; DB 1; Length 396; 73.7%; Pred. No. 1.6e-05; 13.7%; Pred. S. Mismatches 3; Indels 13.9
                                                                                                                                                                                           Burkholderia cepacia (Pseudomonas cepacia).
Bacteria: Proteobacteria: beta subdivision:
                                                                                                                                                                                                                                                                                                                                                      ;
                                                       83.3%; Score 75; DB 1; Length 391; 78.9%; Pred. No. 1e-05;
                     GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 036718E6A48B48A9 CRC64;
                                                                                                                                                           01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                           1; Mismatches
                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                  19 26 GTII
76 80 GTI
131 134 GTI
391 AA; 42713 MW;
                                                                                                1 RGKFERTKPGVNIGTIXXV 19
                                                                                                              3 KGKFERTKPHVNIGTIGHV 21
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                     STANDARD;
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80
134
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                         Complete proteome.
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                                                                                                                                                                                          Matches
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SEQUENCE FROM N.A.

RY STRAIN-CY. Columb pibboed=10617198; R. Murphy G., Volckaert G., Reminer G., Nambutte R., Marpet R. F. T., Schoeft A., Stlekema W., Stitlank. D., Terfyn N., Mayer K.F. Y., Schoeft A., Stlekema W., Stitlank. D., Terfyn N., Mayer K.F. Y., Schoeft A., Stlekema W., Schoeft R., Maclie R., Marche R., March R., Barache M., Schmidthein T., March B., Barache M., Schmidthein T., March B., Barache M., Schmidthein T., March Barcher J., Schoeft B., Baricher H., Ridley P., Hohelsel J., MacCull B., Billham L., March Robben J., Vandenbussche F., Rangham S., A., McCull Grymonprez B., Churst R., Aert R., Deffor E., Rangham J., March Robben J., Vandenbussche F., Rangham S., March R., Britan H., Matly B., Billham L., March R., March R
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Nature FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF -1- FUNCTION: THIS PROTEIN AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES
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MFDL/INE=90190846; PubMed=2314461;
Macture=90190846; PubMed=2314461;
Macture S.L., Palamer J.D.;
Macture 344:262-265(1990).
                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence of EF-Tu).
17-OCT-2001 (Rel. 40, Chorplast precursor (EF-Tu).
18-Indiation (Rouse-ear cress).
17-OCT-2001 (Rel. 40, Rept.)
17-OCT-2001 (Rel. 40, Rept.)
18-Indiation (Mouse-ear cress).
18-Indiation (M
476 AA.
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1 RGKFERTKPGVNIGTIXXV 19
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hes 15; Conservative
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                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, JQ2240; JQ2240.
PIR; S46548; S46548.
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478 AA;
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NP_BIND
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way entities requires a license agreement is not removed. Usage by and for commercial or send an email to licenseagreement (see http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana sylvestris (Wood tobacco).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicottyledons; core eudicots;

NCBI_TaxID=4097, 4096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 72; DB 1; Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-N. Laborum: STRAIN-CV. NK 236;
MEDLINE-94105295; PubMed-8278500;
Ursin V.M., Becker C.K., Shewmaker C.K.;
"Cloning and nucleotide sequence of a tobacco chloroplast translational elongation factor, EF-Tu.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6041F540224A1738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PSO0301; EFACTOR_GTP; 1
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor Tu, chloroplast precursor (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                        EMBL; AL080233; CAB45802,2; PRBL; AL080233; CAB79036.1; PRF; S09152; S09152; PRSP; PD2990; LEU SWISS-2DPAGE; P17745; ARATH. InterPro; IPR004160; EFTU_CTEPRO; IPR004160; EFTU_CTEPRO; IPR004161; IPR004161
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00009; GTP_EFTU. 1
Pfam: PF03143; GTP_EFTU. 1
Pfam: PF03144; GTP_EFTU.D3; 1
PRINTS: PR00315; ELONGARNECT.
TIGREAMS: TIGR00231; Small_GTP; 1
TIGREAMS: TIGR00485; EF-TU: 1.
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000795; EF_GTPbind.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 93 GTP
148 152 GTF
203 206 GTF
476 AA; 51630 MW; 6
                                                                                                                                                                                                                       EMBL; X52256; CAA36498.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transit peptide; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11111 | 111111 | 1
70 RGKFERKKPHVNIGTIGHV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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SEQUENCE
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                              -!- SUBCELLULAR LOCATION: Chloroplast,
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota:
Bukaryota:
Spermatophyta: Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478 ELONGATION FACTOR TU.
95 GTP (BY SIMILARITY).
208 GTP (BY SIMILARITY).
51956 MW; 98116E09E5FACCO1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00301; EF-TU.
Ef-Drogation factor; Protein biosynthesis; GTP-binding;
Transit peptide; Chioroplast.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outstory,
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu, chloroplast precursor (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 72; DB 1;
78.9%; Pred. No. 4.3e-05
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 AA.
SPECIES=N.Sylvestris;
MEDLINE=94373864; PubMed=8087886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPRO04541, EF-Tu.
InterPro: IPRO04165, EFTU.Cterm.
InterPro: IPRO04161, EFTU.D2.
InterPro: IPRO04054, EF-Tu.D2.
InterPro: IPRO05255, Small.GTP.
Pfam: PF00109, GTP_EFTU; I.
Pfam: PF00104; GTP_EFTU.D3; I.
Pfam: PF00144; GTP_EFTU.D3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03144; GIE. S. C. PRINTS; PR00315; ELONGATNFCT.
TIGREAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                         EMBL; M94204; AAA18546.1; -. EMBL; D11469; BAA02027.1; -.
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EFTU_EIKCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
       STRAIN=CV. Maple Arrow; TISSUE=Leaf;

Bonny C., Stutz E.;

"Soybean (Glycine max 1.) nuclear DNA contains four tuf genes conding
"Soybean (Glycine max 1.) nuclear DNA contains four tuf
for the chloroplast specific translation elongation factor EF-Tu.";
for the chloroplast specific translation elongation factor EF-Tu.";
Chimia 47:247-249(1993).

"FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOCALL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                         -i- SUBCELLULAR LOCATION: Chloroplast.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Ceresia; Murone M., Stutz E.; Murer F., Murone M., Stutz E.; Tructure and differential The tuf gene family of soybean: structure and differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72; DB 1; Length 479;
Pred. No. 4.3e-05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 96 GTP (BY SIMILARITY)

151 155 GTP (BY SIMILARITY)

206 209 GTP (BY SIMILARITY)

308 333 N-LINKED (GLCNAC. P) (PA

479 AA; 52095 MW; 43C97B99EACF4971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor Tu, chloroplast precursor (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lon factor; Protein biosynthesis; GPP-binding; peptide; Chloroplast; Multigene family.

1 71 FLOROPLAST (POTENTIAL).
72 479 ELONGATION FACTOR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGREAMS; TIGRO0231; Small_GTP; 1. TIGREAMS; TIGRO0485; EF-Tu; 1. PROSITE; PS00301; EFACTOR_GTP; IS PROSITE; PS00301; Protein blosyntle
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO04541; EF-Tu.
InterPro; IPRO04160; EFTU_Cterm.
InterPro; IPRO04161; EFTU_D2.
InterPro; IPRO00795; EF_GFPbind.
InterPro; IPRO05225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00009; GTP_EFTU.1.
Pfam; PF03144; GTP_EFTU_D3; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 RGKFERKKPHVNIGTIGHV 91
                                                                                                                                                                                                                                                                                                                                                                EMBL; X66062; CAA46864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression.";
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SEQUENCE
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TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 23834;
MEDLINE=9332781; PubMed=8473870;
Rao V.K., Whitlock J.A., Progulske-Fox A.;
"Cloning, characterization and sequencing of two haemagglutinin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Eikenella.
NCBI_TaxID=539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Eikenella corrodens."; J. Gen. Microbiol. 139-650(1993).
J. Gen. Microbiol. 139-639-650(1993).
-I. FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL. TRIA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                       -i-SUBCELLULAR LOCATION: Chloroplast.
-i-SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/FF-IA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
Plant Sci. 117:83-92(1996).
-i- FUNCTION: THIS PROPERN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-FENA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
, CD65F0E262BBD77B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00301; EFACTOR_GTP; 1. PROSITE; PS00301; Protein biosynthesis; GTP-binding; Elongation factor; Protein biosynthesis; GTP-binding; Pransit peptide; Chloroplast; Multigene family Transit peptide; Chloroplast; CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 1; I
Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
11-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                          151 155 G7
206 209 G7
479 AA; 52509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 RGKFERKKPHVNIGTIGHV 91
                                                                                                                                                                                                                                                                                                                                                  EMBL; X89058; CAA61444.1; -.
HSSP; P02990; 1EFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
155
209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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2 08:51:22 2003 Fri May

us-09-810-764a-5.rsp This SWISS-PROT entry is copyright. It is produced through a collaboration the Busins institute of Bioinformatics and the EMBLO dustable of Drope of the EMBL outstation modified and this statement is not removed. There are no restrictions on the entities requires a license agreement (See http://www.isb-sib.ch/announce/mww.green.com.entities. -!- SIMILARIY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. 77.8%; Score 70; DB 1; Length 46; Pred. No. 8.2e-06; 3; Mismatches 3; Indels EMBL; 21261U; Chairer. IR; \$23851; \$23851. InterPro; PR0000755; EF_GTPbind. PROSITE; P80001; EFPCTOR_GTP; I. Elongation factor; Protein biosynchesis; GTP-binding. 46 AA; 4819 MW; 9FFA8E6791379235 CRC64; Local Similarity 68.48 Query Match

Matches

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               0; Gaps
                                                                                                                                                                                                                                                                                                                                        -i- balonanabalo.
-i- SUBCELLUGAT LOCATION: Chloroplast.
-i- SIMILARIYE BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                              Eukāryotā, stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
                                                                                         Last sequence update)
Last annotation update)
                                                                      PRT; 409 AA.
                                                                                                             odontella sinensis (Marine centric diatom).
                                                                    1 RGKFERTKPGVNIGTIXXV 19
           Interpro; IPRO0454; EF-Tu.
Interpro; IPRO04160; EFTU.
Interpro; IPRO04061, EFTU.
Interpro; IPRO00505; EFTU.D2
Interpro; IPRO05255; EFTU.D2
Pfam; PF00009; GTP_EFTU; I.GTP.
                                                              STANDARD;
                                                         P49462
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BIOSYNTHESIS.

SUBCELLULAR LOCATION: Chloropiast.

SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

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                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            MEDDING-939864; PubMed=10468594; Turmel M., Otis C., Lemieux C.; Otivacea; insights into the architecture of the green alga Nephroselmis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
                                                                                                                                                                 , bb 1,
...a. 8.3e-05,
...a. 4; Indels
                                                                                                                                                                   Length 409;
                                                                                                     GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GW, 3DBBBRAC190C2009 CRC64;
PFam; PF03143; GTP_EFTU_D3; 1.
PFam; PF03144; GTP_EFTU_D2; 1.
TIGRPAMS; TIGRO0231; EFTU_D2; 1.
TIGRPAMS; TIGRO0231; EFTU; 1.
FIGRPAMS; TIGRO0485; EPTU; 1.
ELONGATIC; PFOTU; 1.
ELONGATIC; PFOTU; 1.
ELONGATIC; Protein blosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                       Viridiplantae: Chlorophyta; Prasinophyceae;
rales; Chlorodendraceae; Nephroselmis.
                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
115-JUN-2002 (Rel. 41, Last sequence update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                Mismatches
                                                                                                                                            llarity 77.8%; Score 70; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                       PRT;
                                                                                        19 26 GTF
81 85 GTF
136 139 GTF
409 AA, 44560 MW, TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PPO0009; GTP_ERTU. 1.

Pfam: PR03143; GTP_ERTU. 1.

Pfam: PR03144; GTP_ERTU_D3; 1.

PRINTS; PR00315; ELONGATNECT.

TIGREAMS; TIGR00231; Small_GTP; 1.
                                                                                                                                                                                1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                               Interpro; IPR00454; EF-Tu,
Interpro; IPR004160; EF-Tu,
Interpro; IPR004161; EFTU,
Interpro; IPR004161; EFTU_D2
Interpro; IPR00795; EF_GTPD.ind
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                    Local Similarity
les 15; Conserv;
                                                                                                                                                                                                                                                                                                                             Nephroselmis olivacea.
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridipl
Chlorodendrales;
NCBI_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                   NP_BIND
NP_BIND
NP_BIND
SEQUENCE
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09TKZ5;
                                                                                                                                       Query Match
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DR
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CONFLICT
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-:- SUBCELLUIT: MONOMER (CALONITARITY).
-:- SUBCELLUIT: BELONGS TO THE GIP-BINDING ELONGATION FACTOR FAMILY.
-:- SIMILARITY: BELONGS TO THE GIP-BINDING ELONGATION FACTOR FAMILY.
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Mature 396:133-140(1998). PROMOTES THE GTP-DEPENDENT BINDING OF NATURE 396:133-140(1998).

IEUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT PROTEIN ATURE AMINGANTL. TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Wadrid E; pubMed-8892818; Andersson S.G.E., Kurland C.G.; MEDLINE-97041977; pubMed-8892818; Andersson S.G.E., Kurland C.G.; SYGDINEN A., Amiri H., Jamal A., Andrin H., Genes in Rickettsia Syvanen A., Aniri H., Jamal A., Andrin A., Aniri H., Jamal A., Animeric disposition of the elongation factor genes in Rickettsia A. Animeric disposition of the elongation factor genes in Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fickettsia prowazekii. alpha subdivision; Rickettsiales; Bacteria, proteobacteria; Rickettsia. Rickettsiaces; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                        GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
A7A9B0A6E99C1B23 CRC64;
                                                                                                                                    PROSITE; PS00301; EFACTOR_GTP; 1. Thesis; Chloroplast; Elongation factor; Protein biosynthesis; Chloroplast; Crionation factor; Protein biosynthesis; Chloroplast; Crional factor; Protein bionation of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 39, Last sequence update)
13-007-2000 (Rel. 40, Last annotation update)
16-007-2001 (Rel. 40, EF-Tu)
FINGALE factor Tu (EF-Tu)
TUF OR RP661.
                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%; Score 70; DB 1; 178.9%; Pred. No. 8.3e-05; 78.9%; pred. No. 8.3e-05; tive
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INCEPPO: IPRO04454; BFTU_CCETT.
INCEPPO: IPRO04161; BFTU_D2.
INCEPPO: IPRO0795; BE_GTPDind.
INCEPPO: IPRO05225; SMall_GTP.
INCEPPO: IPRO05225; SMall_GTP.
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ЕМВЬ; АJ235272; САА15101.1; -.
HSSP; P02990; 1ETU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jwazekii."; 178:6192-6199(1996).
Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
2 08:51:22 2003
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136 139
410 AA; 44810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGKFERTKPGVNIGTIXXV 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.95
Best Local Similarity 78.95
Best Local Similarity 78.95
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P48865;
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SEQUENCE
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-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SUBCELLULARITY: BELONG. TO THE GIP-BINDING ELONGATION FACTOR FAMILY.
-1- SIMILARITY: BELONG.
-1- SIMILARITY: BELONG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bruex A.; \theta_{\rm c}, Heinrich-Heine University / Duesseldorf, Germany-Thesis (1994), Heinrich-Heine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Serovar 3; Pubmed-11048724; J.S., Heiner C.R., Chen B.Y., MEDLINE-20500319; Pubmed-11048724; G.S., Heiner C.R., Chen B.Y., Glass J.I., Lefkowltz B.J., Glass J.B., Leftwork B.J., Glass J.B., Glass J.B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                             GTP (BY SIMILARITY).
GTP (BX SIMILARITY).
GTP (BX SIMILARITY).
STP (BX SIMILARITY).
STP (BX SIMILARITY).
STP (BX SIMILARITY).
STP (STP SIMILARITY).
STP STP STP SIMILARITY.
W; 510FB299TE389BBF CRC64;
Pram; PF03143; GMP_EFTU_D3; 1.
Pram; PF03144; GTP_EFTU_D2; 1.
Pram; PF03145; ELOGATNECT.
TIGREAMS; PTGC00231; small_GTP; 1.
TIGREAMS; TIGRO0485; EFF-TO, 1.
TIGREAMS; TIGRO0485; EFF-TO, 1.
PROSTE; PS00301; EFRCTOR_GTP; 1.
ELOGATION_ICCTO; PLOTEIN biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUCUT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, EF-TU)
Elongation factor TU (EF-TU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.7%; Score 69; DB 1; 1
73.7%; Pred. No. 0.00012;
73.7%; Pred. No. 4;
tive
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InterPro; IPR004160; BFTU_Cterm.
InterPro; IPR004161; BFTU_DD.
InterPro; IPR000795; BF_GTPbind.
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EMBL; AE002151; AAF30935.1;
HSSP; P02990; LETU.
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198 198 R
205 207 MW;
394 AA; 42921 MW;
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Local 14; Conservative
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198
207
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SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stearothermophilus.";
J. Mol. Biol. 283:371-381(1998).
- FUNCTION: THIS PROPER PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krasny L., Mesters J.R., Tieleman L.N., Kraal B., Fucik V.,
Hilgenfeld R., Jonak J.,
"Structure and expression of elongation factor Tu from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                  19 26 GTP (BY SIMILARITY).

81 85 GTP (BY SIMILARITY).

136 139 GTP (BY SIMILARITY).

394 AA; 42902 MW; 80A887BGC59883E0 CRC64;
                       Pfam; PF00009; GTP_FFTU, 1.
Pfam; PF03143; GTP_EFTU, 1.
PRINTS; PR03144; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNECT.
TIGREPAMS; TIGR00231; small_GTP; 1.
PIGREPAMS; TIGR00485; EF_TU; 1.
PROSITE; PF0301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 1; Pred. No. 0.00012; 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 395 AA.
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InterPro: IPR004541; EF-Tu.
InterPro: IPR004160; EFTU_Cterm.
InterPro: IPR004161; EFTU_D2.
InterPro: IPR00795; EF_GTPbind.
InterPro: IPR005225; Small_GTP.
Pfam; PP00009; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D3; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CCM 2184;
MEDLINE=98443240; Pubmed=9769211;
InterPro; IPR005225; Small_GTP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
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                                                                                                                                                                                                                                                                              Complete proteome.
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050306;
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NP_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROPEIN PROMOFES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPAIN-ATCC 13059 / AS019;
MEDLINE-94368062; PubMed-8085791;
Ludwig W., Neumaiar J., Klugbauer N., Brockmann E., Roller C.,
Klugbauer S., Reetz K., Schachtner I., Ludwigsen A.,
Bachleitner M., Fischer U., Schleifer K.H.;
"Phylogenetic relationships of Bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SUBGNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLIAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                    ó
                                                                                                                                                                                           76.7%; Score 69; DB 1; Length 395; 73.7%; Pred. No. 0.00012; tive 1; Mismatches 4; Indels
TICRFAMS, TIGRO0485, EF-Tu; 1.

PROSITE; PS00301; EFACTOR_GTP; 1.

Elongation factor; Protein blosynthesis; GTP-binding.

NP_BIND 19 26 GTP (BY SIMILARITY).

"" RIND 81 85 GTP (BY SIMILARITY).

"136 GTP (BY SIMILARITY).

"176 GTP (BY SIMILARITY).

"177 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum (Brevibacterium flavum).
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
TUF OR CGL0497.
                                                                                                                                                                                                                                                                                                                                                                                                       396 AA.
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STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antonie Van Leeuwenhoek 64:285-305(1993).
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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EMBL, AP005275; BAB97890.1; -.
HSSP; P02990; LETU.
InterPro; IPR004541; EF-Tu.
InterPro; IPR004160; EFTU_Cterm.
InterPro; IPR000161; EFTU_D2.
InterPro; IPR000795; EF_GTPbind.
InterPro; IPR000525; Small_GTP.
Pfam; PF00009; GTP_EFTU; 1.
                                                                                                                                                                                                                                                                     1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                         Local Similarity 73.77 tes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                               EFTU_CORGL
P42439:
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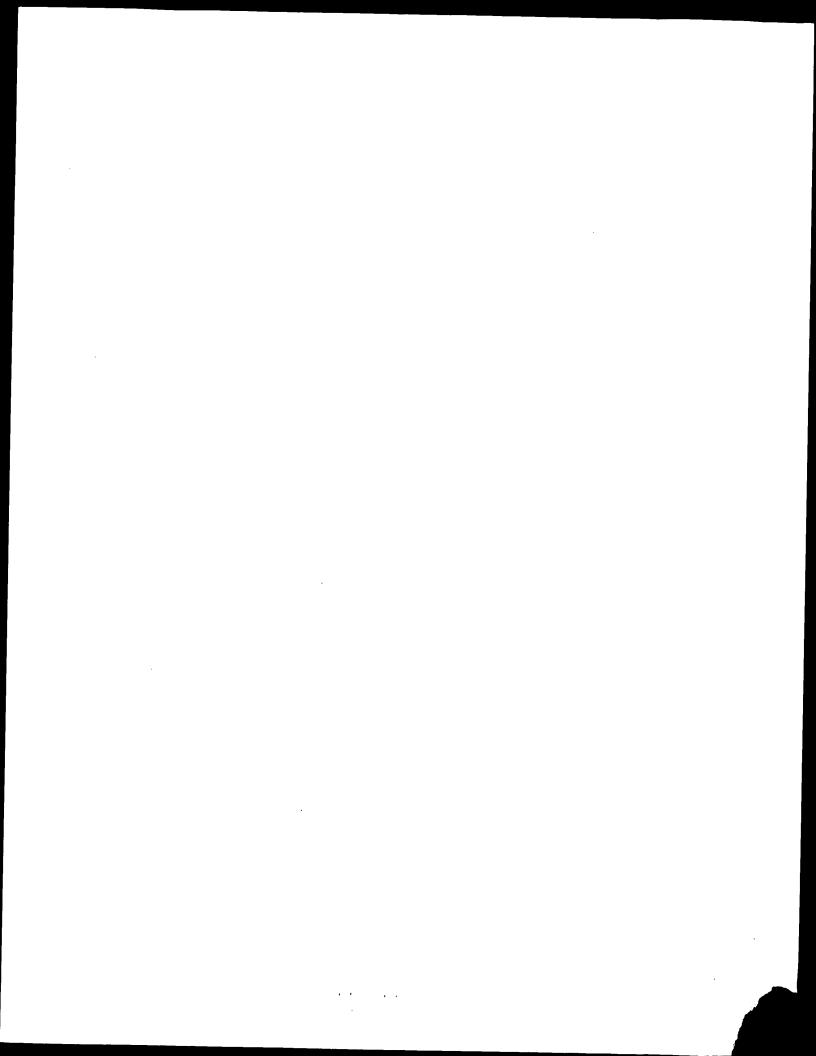
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-93188701; PubMed-8446028;
MEDLINE-93188701; PubMed-8446028;
Honore N.T., Bergh S., Chanteau S., Doucet-Populaire F.,
Eiglameier K., Garnier T., Georges C., Launois P., Limpaiboon T.,
Newton S., Niang K., del Portillo P., Ramesh G.R., Reddi P.,
Ridel P.R., Sittisombut N., Wu-Hunter S., Cole S.T.;
"Nucleotide sequence of the first cosmid from the Mycobacterium
leprae genome project: structure and function of the Rif-Str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94375410; PubMed-8089081; Dhanddyuthapani S., Banu J.M., Kashiwabara Y.; "Cloning and sequence determination of the gene coding for the elongation factor Tu of Mycobacterium leprae."; J. Biochem. 115:664-669(1994).
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silbak F., Bercovier H.;
"Nucleotide sequence of Mycobacterium leprae elongation factor
                                                                                                                                                                                                            76.7%; Score 69; DB 1; Length 396; 73.7%; Pred. No. 0.00012;
                                                                                                                                                                                                                                             4; Indels
                                                                                                                       GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; F46333EC113AB5FD CRC64;
                                                    TIGRFAMS; TIGR00231; small_GTP; 1.
TIGRFAMS; TIGR00485; B-Tu; 1.
FROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Massive gene decay in the leprosy bacillus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (FF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 396 AA.
                                                                                                                                                                                                                                Pred. No. 0.00
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microbiol. 7:207-214(1993).
Pfam; PF03143; GTP_EFTU_D3; 1. Pfam; PF03144; GTP_EFTU_D2; 1. PRINTS; PR00315; ELONGATNFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                            138 141 G
396 AA; 43852 MW;
                                                                                                                                                                                                                                                                                1 RGKFERTKPGVNIGTIXXV 19
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nes 14; Conserva
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EFTU_MYCLE
                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVPYILVALNKSDAVDDEELLELV -> VYLTSWSHLTSPT
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                                                         -!- SUBGNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=53446;
NATUTE 409:1007-1011(2001).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWTTRNYSSLS (IN REF. 2).
L -> V (IN REF. 2).
C -> A (IN REF. 2).
R -> P (IN REF. 3).
D9CB88343C642778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elongation factor; Protein biosynthesis; GTP-binding;
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GTP (BY SIMILARITY)
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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TIGRFAMS; TIGRO0485; EF-TU; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004161; EFTU_D2.
InterPro; IPR000795; EF_GTPbind.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                              EMBL; L13276; AAA71969.1; -.
EMBL; Z14314; CAA78674.1; -.
EMBL; D13869; BAA02982.2; -.
EMBL; AL583923; CAC30831.1; -.
PIR; S34954; S34954.
                                                                                                                                                                                                                                                                                                                                                                                           EFTU_Cterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43667 MW;
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                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004541; EF-Tu.
InterPro; IPR004160; EFTU_C
                                                                                                            EF-TU/EF-1A SUBFAMILY.
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152
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les 14; Conserv
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                                                 BIOSYNTHESIS.
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                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                       -i-SUBCELLULAR LOCATION: Cytoplasmic.
-i-SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.7%; Score 69; DB 1; Length 397; Best Local Similarity 73.7%; Pred. No. 0.00012; Matches 14; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elongation factor; Protein blosynthesis; GTP-binding. NP_BIND 19 26 GTP (BY SIMILARITY). NP_BIND 83 87 GTP (BY SIMILARITY). NP_BIND 138 141 GTP (BY SIMILARITY). SEQUENCE 397 AA; 43891 MW; EEB8235730DBBBB7 CRC64;
                                                                                    SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PÉGAN, PRÓ0109; GTP_EFTU; 1.
PÉGAN, PRÓ0143; GTP_EFTU_D2; 1.
PÉGAN, PRO03144; GTP_EFTU_D2; 1.
PKINTS; PRO0315; ELONGATNECT.
TICRFAMS; TIGRO0241; SMB1LGTP; 1.
TICRFAMS; TIGRO0485; EF-TU; 1.
PROSITE; PSO0301; EFACTOR_GTP; 1.
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Interpro; IPR004160; EFTU_Cterm.
Interpro; IPR004161; EFTU_Cterm.
Interpro; IPR0007165; EF_GTPbind.
Interpro; IPR000795; EF_GTPbind.
Interpro; IPR005225; Small_GTP.
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Search completed: April 29, 2003, 09:40:54

Job time : 26 secs



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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein . protein search, using sw model

Run on:

April 29, 2003, 09:36:44 ; Search time 29 Seconds (without alignments) 134.996 Million cell updates/sec

Perfect score:

US-09-810-764A-5 90 1 RGKFERTKPGVNIGTIXXV 19 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_unclassified:* sp_human:*
sp_invertebrate:*
sp_mammal:* sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:* sp_organelle:* sp_phage:* sp_plant:*
sp_rodent:* sp_virus:* sb_mhc:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	Description		Oyserg oryza sativ	U8W2C3 Oryza sativ	Q919s8 edta-degrad	OByp63 anabaena sp	Q40450 nicotiana s	O9axu2 pelargonium	043364 nicotiana s	Ogyhp2 brucella me	Q933r9 ureaplasma	Q92gw4 rickettsia	O9rg55 streptomyce	Q8yhq4 brucella me	Q9rg53 streptovert	Q93t39 streptomyce	007005 0100+0010	Od+1v8 Crost Idium	ASCEAGE CYALLUM C
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	Score	78	78	75	72	72	72	72	69	69	69	69	69	89	6.8	63	2 (67	
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	O9x091 COXIELLA DU O9x420 porphyromon
09KV37 08ZJB2 08ZAD8 08ZAD8 08XZSD9 08XGZD9 08KTV2 08KTV2 09KTV2 09ZD5 09ZD5 09ZD7 09ZB1 0	Q9R420
100 100 100 100 100 100 100 100 100 100	
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	395
73.3 73.3 73.3 73.3 73.3 73.3 772.2 772.2 772.2 772.2 772.2 772.2 772.2 772.2 772.2 772.2 773.3	7
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ALIGNMENTS

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STRAIN=BNC1
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Q8YP63
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Schouslavek J., Payne J.W., Liu Y., Bolton H. Jr., Xun L.;
"Cloning, Sequencing, and Characterization of a Gene Cluster Involved in EDTA Degradation from the Bacterium BNC1.";
Appl. Environ. Microbiol. 67:688-695(2001).
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                                               Gaps
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A Lee J.-H., Kim J.-K.;

Lee J.-H., Kim J.-K.;

Lee J.-H., Kim J.-K.;

The Chloroplast translational elongation factor Tu gene of rice.";

"Chloroplast translational elongation factor Tu gene of rice.";

"Interpose the Company of the EmbL/GenBank/DDBJ databases."

"Interpose the Rod 18-Tu L.

"Interpose the R
                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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    86.7%; Score 78; DB 10; Length 467; 84.2%; Pred. No. 2.3e-05; Live 0; Mismatches 3; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                             Q8W2C3;
01-MAR-2002 (TrEMBLrel. 20, Created)
11-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Translational elongation factor Tu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 391 AA.
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                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDTA-degrading bacterium BNC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RGKFERTKPHVNIGTIGHV 79
                                                                                             1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                  61 RGKFERTKPHVNIGTIGHV 79
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                  Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
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                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                RESULT 2
Q8W2C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9F9S8
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Liu Y., Louie T.M., Payne J., Bohuslavek J., Bolton H. Jr., Xun L.; "Idu Y., Louie T.M., Payne J., Bohuslavek J., Bolton H. Jr., Xun L.; "Identification, purification, and characterization of iminodiacetate oxidase from the EDTA-degrading bacterium BNC1."; Appl. Environ. Nicrobiol. 67:696-701(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Kanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Katanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nasazaki M., Shimpo S., Sugimoto M., Takazawa M., Yamada M., A Makazaki M., Tabata S., Sugimoto M., Takazawa M., Yamada M., A Makazaki M., Tabata S., Sugimoto M., Takazawa M., Yamada M., A Masada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., R. Complete genomic sequence of the filamentous nitrogen-fixing cryanobacterium Anabaena sp. strain PCC 7120."; EMBL; APO05366; BAB76036.1; -.

InterPro: IPR004160; EFTU.Cterm.

InterPro: IPR004161; EFTU.D.2.

InterPro: IPR004161; EFTU.D.2.

InterPro: IPR004161; EFTU.D.2.

InterPro: IPR004161; EFTU.D.2.

InterPro: IPR004163; EFTU.D.3.

InterPro: IPR004163; EFTU.D.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 AA; 42794 MW; E6B41737CCD77AA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Translation elongation factor EF-Tu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 72; DB 16;
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83.3%; Score 75; DB 2; 1
Best Local Similarity 78.9%; Pred. No. 6.5e-05;
Matches 15; Conservative 1; Mismatches 3
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Pfam; PF03143; GTP_EFTU_D3; 1.

PRINTS; PR00315; ELONCAINFCT.

TIGRFAMS; TIGR00485; EF-Tu; 1.

TIGRFAMS; TIGR00231; small_GTP; 1.

PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                 Pfam; PP00009; GTP_EFTU; 1.
Pfam; PP03144; GTP_EFTU_D2; 1.
Pfam; PP03143; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNECT.
TIGRFAMS; TIGR00485; EF-Tu: 1.
TIGRFAMS; TIGR00231; Small_GTP; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21595285; PubMed=11759840;
                                     MEDLINE=21091959; PubMed=11157233;
                                                                                                                                                                                             HSSP, P07157; 1A1P.
InterPro; IPR004541; EF-Tu.
InterPro; IPR004160; EFTU_Cterm.
InterPro; IPR004161; EFTU_D.1.
InterPro; IPR000795; EF_GTPbind.
InterPro; IPR005225; Small_GTP.
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SEQUENCE FROM N.A.
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NCBI_TaxID=73200;
                                                                                                                                                                          Tu cDNA."
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Murayama Y., Matsubayashi T., Sugita M., Sugiura M.;
Purification of chloroplast elongation factor Tu and cDNA analysis in tobacco: the existence of two chloroplast elongation factor Tu
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pelargonium graveolens (rose geranium).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Geraniales; Geraniaceae; Pelargonium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                        01-NOV-1996 (TFEMBLrel. 01, Last sequence update)
01-JUN-2002 (TFEMBLrel. 21, Last annotation update)
Chloroplast elongation factor TuA (EF-TuA) precursor (Fragment).
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                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49732 MW; 8A30C50DC137F755 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chloroplast translational elongation factor Tu.
      Pred. No. 0.00023;
                                                                                                                                                                                                                         457 AA.
78.9%; Prea. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EF-TUA)
                                                                                                                                                                                                                                                             (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                               Nicotiana sylvestris (Wood tobacco).
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lant Mol. Biol. 22:767-774(1993).
                                                                   1 RGKFERTKPGVNIGTIXXV 19
                                                                                                           3 RAKFERTKPHVNIGTIGHV 21
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                        15; Conservative
                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
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  Best Local Similarity
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01-NOV-1996
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                        Matches
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Q40450
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                MEDITNE=20550852; PubMed=11101151; Kang C.J., Lee M.G., Cho Y.S., Lee J.W., Kyung Y.J., Shin J.S., Kim E.S., Kim J.K.; "Characterization of geranium (Pelargonium graveolens) chloroplast EF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murayama Y., Matsubayashi T., Sugita M., Sugiura M.; "Purification of chloroplast elongation factor Tu and cDNA analysis in tobacco: the existence of two chloroplast elongation factor Tu species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugita M., Murayama Y., Sugiura M.; "Structure and differential expression of two distinct genes encoding the chloroplast elongation factor Tu in tobacco."; Curr. Genet. 25:164-168(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eussterids I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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TIGREAMS: TICRO00485; EF-Tu; 1.
TIGREAMS: TICRO00231; small_GTP; 1.
PROSITE: PS00301; EFACTOR_GTP; 1.
Elongation factor; GTP-binding; Protein biosynthesis.
SEQUENCE 474 AA; 51315 MW; A321742468553865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Chloroplast elongation factor TUB(EF-TUB) precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 72; DB 10; 78.9%; Pred. No. 0.00028;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana sylvestris (Wood tobacco).
                                                                                                                                                                   InterPro; 1PR004541; EF-Tu.
InterPro; 1PR004541; EF-Tu.
InterPro; 1PR004161; EFTU_D2.
InterPro; 1PR000161; EFTU_D2.
InterPro; 1PR000795; EF GTPbind.
Pfam; PF000199; GTP_EFTU, 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D3; 1.
PKINTS; PR00315; ELDNGATNECT.
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EMBL: D11470; BAA02028.1; --
EMBL: D11376; BAA01975.1; -.
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InterPro; IPR004160; EFTU_Cterm.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR000795; EF_GTPbind.
InterPro; IPR005225; Small_GTP.
                                                                                                                   Mol. Cells 10:579-583(2000).
EMBL; AF234537; AAK08141.1; -.
HSSP; P02990; 1EFU.
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SEQUENCE FROM N.A.
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                                                                                                               TIGRFAMS; TIGR00485; EF-Tu: 1.
TIGRRAMS; TIGR00231; small_GTP: 1.
PROSITE; PS00301; EFACTOR_GTP: 1.
Elongation factor; GTP-binding; Protein biosynthesis; Transit peptide.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                  POTENTIAL.
CHLOROPLAST ELONGATION FACTOR TUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.7%; Score 69; DB 16; Length 391; 73.7%; Pred. No. 0.00076;
                                                                                                                                                                                                                                                                                                                                                                                                  80.0%; Score 72; DB 10; Length 485; 78.9%; Pred. No. 0.00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 AA; 42604 MW; ED4CDF37183A900E CRC64;
                                                                                                                                                                                                                                                                                                                                          FE88EF5D48B92D29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Protein translation elongation factor Tu (EF-TU).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009518; AAL51936.1; -.
InterPro: IPR004941; EF-Tu.
InterPro: IPR004161; EFTU-D2.
InterPro: IPR007161; EFTU-D2.
InterPro: IPR005255; Small_GTP.
InterPro: IPR005255; Small_GTP.
InterPro: IPR005255; Small_GTP.
InterPro: IPR0144; GTP_EFTU_D2; I.
Pfam; PF03144; GTP_EFTU_D2; I.
Pfam; PF03144; GTP_EFTU_D2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      78.9%; Pred. No. 0.00 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE=20020109; PubMed=11756688;
                                                                                                                                                                                                                                                                                                             (EF-TUB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MAR-2002 (TrEMBLrel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00315; ELONGATNECT.
TIGRPAMS; TIGR00485; EF-Tu; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_DD; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00115; ELONGATNECT.
                                                                                                                                                                                                                                                                                                                                                 485 AA; 52688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KSKFERTKPHVNIGTIGHV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 RGKFERKKPHVNIGTIGHV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.03
Best Local Similarity 78.93
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                   485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                            TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O8YHP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                            CHAIN
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RESULT 9

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Gaps
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MEDLINE=2144074;
PUDMed=11557893;
MEDLINE=21440745;
Sanason D., Rous V., Cossart P., Weissenbach J., Claverle J.-M.,
Sanason D., Roux V., Cossart P., Weissenbach J., Claverle J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                  Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Kong F., Gilbert G.L.; "Genomic based mapping and sequencing of U. parvum and U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF270767; AAK58630.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA; 42918 MW; 4CB4B2D776A5B145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.7%; Score 69; DB 2; 1
73.7%; Pred. No. 0.00077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA
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394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
TIGRFAMS; TIGR00485; EF-Tu:
TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00301; EFACTOR_GTP; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
PRT;
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IPR004161; EFTU_D2.
IPR000795; EF_GTPDind.
IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF270758; AAK58621.1;
EMBL, AF270759; AAK58622.1;
EMBL, AF270760; AAK58623.1;
EMBL, AF270761; AAK58624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF270762; AAK58625.1;
EMBL; AF270763; AAK58626.1;
EMBL; AF270764; AAK58627.1;
EMBL; AF270765; AAK58628.1;
EMBL; AF270766; AAK58628.1;
                                                                                                                                                                                                                                                  Mycoplasmataceae; Ureaplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004541; EF-Tu.
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TUF OR RC1008.
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     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            STRAIN-VARIOUS STRAINS;
                                                                                                                                       Elongation factor Tu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=2130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      urealyticum.";
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                                     Q933R9;
        Q933R9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bactéria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olsthoorn-Tieleman L.N., Claij N., Hilgenfeld R., Kraal B.;
Elongation factor Tul from the pulvomycin producer Streptomyces
mobaraense is resistant to both pulvomycin and kirromycin.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
HSSP; P02990; IRTU.
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0
                                                                                                                                                                                                                                                                                                                                                                             Length 394;
                                                                                                                                                                                                                                                                                                                                                                   76.7%; Score 69; DB 16; Length 39 73.7%; Pred. No. 0.00077; Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.7%; Score 69; DB 2; Length 39, 71.7%; Pred. No. 0.00078; 4; Indels
                                                                                                                                                                                                                                                                                                                      394 AA; 42868 MW; 1FBE465785530C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 AA; 43811 MW; DA439151BFE6BC2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Elongation factor Tul.
                                                                    InterPro; IPR004160; EFTU Cterm.
InterPro; IPR004160; EFTU Cterm.
InterPro; IPR0004161; EFTU Cterm.
InterPro; IPR000795; EF_GFPbind.
InterPro; IPR000795; EFTU D2.
Pfam; PF03144; GTP_EFTU, 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
TIGRRAMS; TIGR00485; EFTU; 1.
TIGRRAMS; TIGR00231; Small_GTP; 1.
PR093TE; PS03001; EFRACTOR_GTP; UNKNOWN_1.
SEQUENCE 394 AA; 42868 WW; IFBE46578530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004541; EF-Tu.
InterPro; IPR004160; EFTU_Cterm.
InterPro; IPR004161, EFTU_LD2.
InterPro; IPR000795; EF GTPbind.
InterPro; IPR005225; Small_GTP.
Pfam, PF00009; GTP_EFTU_1 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGRO0485; EF-Tu: 1
TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                 EMBL; AE008652; AAL03546.1; -.
InterPro; IPR004541; EF-Tu.
Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGKFERTKPGVNIGTIXXV 19
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                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 73.7
hes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces mobaraensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=35621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC29032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP-binding.
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RESULT 12 Q8YHQ4

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Delvecchio V.G., Kapatral V., Rečkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrzhides N., Overbeek R.; The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptoverticillium netropsis (Streptoverticillium flavopersicus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=55404;
                                                                                                                Brucella melitensis.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-TU1063;
Olsthoorn-Tieleman L.N., Claij N., Hilgenfeld R., Kraal B.;
Elongation factor Tul from the pulvomycin producer Streptomyces mobaraense is resistant to both pulvomycin and kirromycin.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
HSMBL, AR153618; ARF22608.1;
HSSP; P02990; 1ETU.
InterPro; IPR004160; EFTU_Cterm.
InterPro; IPR004160; EFTU_Cterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 AA; 44340 MW; 9523841BFF2C08DF CRC64;
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Protein translation elongation factor Tu (EF-TU).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Mall. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009516; AAL51933.1; -
InterPro; IPR004541; EFTU.Cterm.
InterPro; IPR004160; EFTU.Cterm.
InterPro; IPR004161; EFTU.Dz.
InterPro; IPR0040161; EFTU.Dz.
InterPro; IPR0040195; EFGTPbhhd.
InterPro; IPR005225; Small.GTP.
Pfam; PF03144; GTP.EFTU.D3; 1.
Pfam; PF03144; GTP.EFTU.D3; 1.
Pfam; PF03143; GTP.EFTU.D3; 1.
Pfam; PF03143; GTP.EFTU.D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                          STRAIN-16M / ATCC 23456 / BIOTYPE 1;
MEDLINE-20020109; PubMed-11756688;
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TIGREAMS; TIGRO0231; small_GTP; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGKFERTKPGVNIGTIXXV 19
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                                                                                                                                                                 Brucellaceae; Brucella.
NCBI_TaxID=29459;
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Best Local Similarity
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                             BMEI0742.
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Kormanec J., Mouyen L.D., Novotna J., Knirschova R., Weiser J.;

Kormanec J., Mouyen L.D., Novotna J., Knirschova R., Weiser J.;

Kormanec J., Mouyen L.D., Novotna J., Knirschova R., Weiser J.;

Rembi, AFS68184; ARK4131.1; --

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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1894;
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Live 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                            75.6%; Score 68; DB 2; Length 397; 68.4%; Pred. No. 0.0012; tive 2; Mismatches 4; Indels
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                                                                                                                                                                                                        CTP-binding.

Granmence 397 AA; 43682 MW; 5F3A81F3FC42914F CRC64;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Elongation factor Tu (Ef-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Elongation factor Tu.
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                                         Pfam; PF001009; GTP_BFTU, 1
Pfam; PF03144; GTP_BFTU_D2; 1.
Pfam; PF03143; GTP_BFTU_D3; 1.
PRINTS; PR00315; ELONGATNECT.
TICRFAMS; TIGR00485; EF-TU; 1.
TICRFAMS; TIGR00231; small_GTP; 1.
InterPro; IPR000795; EF_GTPbind InterPro; IPR005225; Small_GTP.
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Matches 13; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Q97EH5;
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097EH5
1D 097EH
AC 097EH
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
OR CAC310
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Q93T39
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us-09-810-764a-5.rai

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 09:39:04; Search time 29 Seconds (without alignments)

Title: US-09-810-764A-5

Perfect score: 90
Sequence: 1 RGKFERTKPGVNIGTIXXV 19
Scoring table: BLOSUM62

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 2000000000

Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Database

	Description	Sequence 3, Appli	, 4	ی :	'n	2 .	Ŋ	24	1,7	23.	25,	189	331,	2. At	i i	148	۳,	'n	'n	124	m	138	9	17	6. At	36,	2.7	331
SUMMARIES	. QI	US-09-140-466-3	US-09-140-466-4	-09-140-	US-09-140-466-5	-09-218-197-	US-09-134-001C-5377	US-08-764-100-24	.US-07-973-431B-1	US-09-254-465A-23	US-09-254-465A-25	US-09-188-930-189	-930-33	US-09-462-270-2	US-09-254-465A-1	US-08-444-818-148	08-443-260-3	US-08-442-805A-3	US-08-443-900A-3	US-08-444-818-124	US-08-249-843-3	444	US-08-833-678A-6	US-08-444-818-177	US-08-529-169A-6	US-08-152-019A-36	US-09-140-466-2	US-09-134-001C-3316
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de (Match	75.6	74.4	73.3	61.1	53.3	53.3	•	•	43.3	43.3	43.3	43.3	43.3	43.3	•	43.3	43.3	•	•	•	43.3	43.3	43.3	•	42.2	42.2	42.2
	Score	89	67	99	52	48	48	41	40	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	38	38	38
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Sequence 2, Appli Sequence 30, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli	THE PLASTID DNA OF THE IN SYNTHESIS INHIBITORS COMPOUNDS	Length 409; ; Indels 0; Gaps 0;	E PLASTID DNA OF THE YNTHESIS INHIBITORS POUNDS
1.12 2 US-08-714-402-2 1.61 4 US-09-327-536-2 330 2 US-08-997-080-30 330 2 US-08-997-362-30 330 4 US-09-09-26-85-30 330 4 US-09-09-24-542-30 330 4 US-09-205-426-30 330 4 US-09-205-426-30 330 4 US-09-205-426-30 239 4 US-09-205-426-2 239 4 US-09-876-85-502-2 239 4 US-09-871-85A-2 239 4 US-09-709-126-2	LIGNMENTS IN ENCODED ON T FE AND PROTEIN NTI-MALARIAL CC 140,466	6%; Score 68; DB 4; 7%; Pred. No. 0.0012; 0; Mismatches 5 19	RESULT 2 US-09-140-466-4 US-09-140-466-4 Sequence 4, Application US/09140466 Sequence 6, Application US/09140466 Retent No. 6568160 GENERAL INFORMATION: APPLICANT: CLOUGH, BARBARA APPLICANT: CLOUGH, BARBARA TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DN TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INH TITLE OF INVENTION: EFEECTIVE AS ANTI-MALARIAL COMPOUNDS FILE REFERENCE: N68837B GCW PJC DP CURRENT APPLICATION NUMBER: US 60/056,246 BARLIER APPLICATION UNBER: US 60/056,246 BARLIER FILING DATE: 1997-08-28 NUMBER OF SEQ ID NOS: 14
28 38 42.2 1 29 38 42.2 1 30 37 41.1 31 37 41.1 31 37 41.1 31 37 41.1 31 37 41.1 31 37 41.1 37	RESULT 1 US-09-140-466-3 Sequence 3, Application US/09140466 Patent No. 6268160 GENERAL INFORMATION: APPLICANT: CLOUGH, BARBARA APPLICANT: CLOUGH, BARBARA TITLE OF INVENTION: AN EF-TU PROTE TITLE OF INVENTION: AN EF-TU PRODE CURRENT APPLICATION WHBER: US/09/CURRENT FILING DATE: 1998-08-26 EARLIER PELERKNE: NG 808.75 B GGW PUC CURRENT FILING DATE: 1997-08-28 NUMBER OF SEQ ID NOS: 14 SSOFTWARE: PATENT SEQ ID NO 3 LENGTH: 409 TYPE: PRT CRANISM: Anacystis nidulans US-09-140-466-3	Query Match Best Local Similarity 73. Matches 14; Conservative Qy RGKFERTKPGVNIGTIXXV	RESULT 2 US-09-140-466-4 Sequence 4, Application Patent No. 6268160 GENERAL INFORMATION: APPLICANT: CLOUGH, BARB APPLICANT: WILSON, ROBE TITLE OF INVENTION: AN TITLE OF INVENTION: AN TITLE OF INVENTION: AN TITLE OF INVENTION: AN CURRENT APPLICATION NUM CURRENT APPLICATION NUM CURRENT FILING DATE: 19 EARLIER APPLICATION NUM CURRENT FILING DATE: 19 EARLIER APPLICATION NUM CURRENT FILING DATE: 19 EARLIER FILING DATE: 19

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Gaps

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6; Indels

1; Mismatches

61.1%; Score 55; DB 4; Length 409; 63.2%; Pred. No. 0.17;

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1 RGKFERTKPGVNIGTIXXV 19
Query Match 61.19
Best Local Similarity 63.29
Matches 12; Conservative
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APPLICANT: CLOUGH, BARBARA

APPLICANT: CLOUGH, BARBARA

APPLICANT: PREIGER;

TITLE OF INVENTION: MALETT PRACEIR SANTI-MALARIAL COMPOUNDS

TITLE OF INVENTION: MALETTIVE DE SANTI-MALARIAL COMPOUNDS

TITLE OF INVENTION: EFFECTIVE BAS SANTI-MALARIAL COMPOUNDS

TITLE OF INVENTION WUMBER: US/09/140,466

CURRENT FILING DATE: 1994-08-26

EARLIER FILING DATE: 1997-08-28

WUMBER OF SEQ ID NOS: 14

SEQ ID NO 6

LENGTH: 394
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APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: WILSON, ROBERT
TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: BEFECTIVE AS ANTI-MALARIAL COMPOUNDS
FILE REFERENCE: N68937B GGW PJC DP
CURRENT APPLICATION NUMBER: US/09/140,466
EARLIER APPLICATION NUMBER: US/09/140,466
EARLIER APPLICATION NUMBER: US/09/140,466
EARLIER PETING DATE: 1998-08-26
EARLIER PILING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 14
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Pred. No. 0.0025;
1; Mismatches 3; Indels
                                                                                                                                      Query Match 74.4%; Score 67; DB 4; Length 408; Best Local Similarity 73.7%; Pred. No. 0.0017; Matches 14; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09140466 Patent No. 6268160
                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09140466
Patent No. 6268160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Cyanophora paradoxa
US-09-140-466-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.38;
76.58;
                                                                                                                                                                                                                         1 RGKFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                              3 RDKFERSKPHVNIGTIGHV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Escherichia coli
US-09-140-466-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KFERTKPHVNVGTIGHV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 76.5
Matches 13; Conservative
      SOFTWARE: Patentin Ver. 2.1
                                                              ; TYPE: PRT
; ORGANISM: Cryptomonas phi
US-09-140-466-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TYPE: PRT
                      SEQ ID NO 4
LENGTH: 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-140-466-5
                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-140-466-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Sequence 5377, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF 
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Pred. No. 2.5;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%; Score 48; DB 4; Length 394; 58.8%; Pred. No. 2.3;
                                                                                                                                                                                                                        US-09-218-197-2
Sequence 2, Application US/09218197A
Sequence 2, Application US/09218197A
Sequence 2, Application US/09218197A
GENERAL INCRATION:
APPLICANT: Kallender, Howard
APPLICANT: Van Horn, Stephanie
TITHE OF INVENTION: EF-TU
FILE REFERENCE: GM10185
CURRENT APPLICATION NUMBER: US/09/218,197A
CURRENT FILING DATE: 1998-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 394
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 24, Application US/08764100
; Patent No. 5773700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.3%;
58.8%;
3 RQKFDGNKPHVNIGTIGHV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 KFDRSKEHANIGTIGHV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 58.8
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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US-09-134-001C-5377
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APPLICANT: ASIMEMALI, ANIMEMALI, ANIMEMALI, ANIMEMIAL, ANIMEMALI, ANIMEMIAL, ANIMEMALI, ANIMEMALI, ANIMEMALI, ANIMEMALI, ANIMEMAL GODGARD, AUGREY, AUSTIN L.

APPLICANT: GUAGA, WALY A.

APPLICANT: TUMBS, Daniel

APPLICANT: Wapier, WARY A.

APPLICANT: Wapier, WARY A.

APPLICANT: Wapier, WASHINDS, COMPOSITIONS AND METHODS FOR THE TREATMENT

TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33-RELATED ANTIGENS

TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33-RELATED ANTIGENS

TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33-RELATED ANTIGENS

TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33-RELATED ANTIGENS

CURRENT APPLICATION NUMBER: US/09/254,465A

PRIOR FILING DATE: 1998-11-20

PRIOR PRIOR APPLICATION NUMBER: US 60/066,364

PRIOR APPLICATION NUMBER: US 60/078,936

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 30

**CHARACTERIZED AND NUMBER: US 60/078,936

**CHARACTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

44.4%; Score 40; DB 1; Length 406;
Best Local Similarity 57.1%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 4; Indels
                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,431B
                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Bisenstein, Ronald I
RECISTATION NUMBER: 30628
RECISTATION NUMBER: 41968
TELEPHONE: (617) 523-3400
TELEPHONE: (617) 523-3400
TELEPHONE: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SUMMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 23, Application US/09254465A; Patent No. 6410708
                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unknown
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| :| ||| :
203 GKFIKTPPGVSAPT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GKFERTKPGVNIGT 15
                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-07-973-431B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-254-465A-23
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                      APPLICANT: Peters, Dirk
APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.6%; Score 41; DB 1; Length 861; 61.5%; Pred. No. 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lu, Yinchen
APPLICANT: Haseltine, William A
TITLE OF INVENTION: YC1 Protein, Gene, And Uses Thereof
TURES OF SUCHENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: David G. Conlin; Dike, Bronstein,
ADRESSEE: Roberts & Cushman
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
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van Grinsven J., Martinus Q.
De Haan, Petrus T.
Gielen L., Johannes J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: US 08/032,235
FILING DATE:
TILING DATE:
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1993
ATORNEY/AGENT INFORMATION:
NAME: NO. 57730015.3
REFERENCE/DOCKET NUMBER: 34,490
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
TELEPHONE: (415) 857-1125
INFORMATION FOR SEG ID NO: 24:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                              ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/07973431B Patent No. 5652144 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 861 amino acids
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US-08-764-100-24
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       94304
                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-973-431B-1
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Gaps

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Gaps
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Ouery Match
43.3%; Score 39; DB 4; Length 260;
Best Local Similarity 58.3%; Pred. No. 47;
Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                       1 RGKFERTKPGVN 12
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MA 02109

STATE:

COUNTRY:

: Homo sapiens

US-09-254-465A-23

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ORGANISM: HOMO SAPIENS US-09-462-270-2
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263 RGHFDRTKKGTS 274
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263 RGHFDRTKKGTS 274
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                                                                                                                 1 RGKFERTKPGVN 12
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US-09-254-465A-1
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LENGTH: 299
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                                                                                                                                                                                 Dp
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                                                                                                                                                                                                                                                 GENERAL INCOMANTION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Condox Sherman
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Goddard, Audrey,
APPLICANT: Wood, William I.
APPLICANT: WOOD, APPLICAN
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Patent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Streachan, Matthew
APPLICANT: Streachan, James Greg
APPLICANT: Murison, James Greg
TILLE OF INVENTION: compositions Isolated From Skin Cells
TILLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.3%; Score 39; DB 4; Length 263; 58.3%; Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                              US-09-254-465A-25; Sequence 25, Application US/09254465A; Patent No. 6410708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50...
7; Conservative
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NAME/KEY: UNSURE
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US-09-188-930-189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || |:||| |:
243 RGHFDRTKKGTS 254
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240 RGHFDRTKKGTS 251
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APPLICANT: Genented
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-188-930-189
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LENGTH: 299
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                                                                                                       RESULT 10
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Gaps
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APPLICANT: SmithKline Beecham Corporation
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Human Flat Antigen: A Cell Surface
TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
FILE REFERENCE: GH-70150US
CURRENT APPLICATION NUMBER: US/09/462,270
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/052,186
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.3%; Score 39; DB 4; Length 299; 58.3%; Pred. No. 54; tive 2; Mismatches 3; Indels
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Query Match
Best Local Similarity 58.3%; Pred. No. 54;
Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                            4; Sequence 331, Application US/09188930A; Patent No. 6150502; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-462-270-2; Sequence 2, Application US/09462270; Patent No. 6358707
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Best Local Similarity 55...
7; Conservative
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Best Local Similarity 55...
7; Conservative
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                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS FILE REPRENCE: P1216R1(US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-13-21
PRIOR FILING DATE: 1998-13-20
PRIOR FILING DATE: 1998-13-20
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
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Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: AF60 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: HATDIN, Aliasa A.
RECISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION:
Sequence 1, Application US/09254465A
                                                                                                           APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
                                                                     Genentech, Inc.
Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.39
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-1
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263 RGHFDRTKKGTS 274
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                                      GENERAL INFORMATION:
                       Patent No. 6410708
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US-08-444-818-148
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LENGTH: 299
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                                                                APPLICANT
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April 29, 2003, 09:41:35; Search time 15 Seconds (without alignments) 101.498 Million cell updates/sec
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_USW_PUB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USO9_USW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Published_Applications_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 247, Apples Sequence 10431, Apples Sequence 10431, Asequence 10431, Asequence 11059, Asequence 1364, Applisequence 1, Applisequence 11415, Asequence 12002, Asequence 12002, Asequence 12002, Asequence 1371, Asequence 5, Applisequence 1371, Asequence 5, Applisequence 1371, Asequence 5, Applisequence 1371, Asequence 5, Applisequence 6, Applisequence 1371, Asequence 6, Applisequence 6, App Sequence 3, Appli Sequence 4, Appli Sequence 6937, Ap Description 0 US-09-845-335-3 0 US-09-845-335-4 0 US-09-912-022-247 0 US-09-815-242-10362 0 US-09-815-242-10362 0 US-09-815-242-11069 0 US-09-815-242-11069 0 US-09-815-242-11069 0 US-09-815-242-11069 0 US-09-815-242-11069 0 US-09-815-242-13964 US-08-831-310-4 0 US-09-815-242-111415 0 US-09-815-242-111995 0 US-09-815-242-12002 0 US-09-815-242-13171 0 US-09-845-335-5 0 US-09-841-132-491 US-09-738-626-6937 US-09-488-737-1 SUMMARIES 8 10 8 Query Match Length DB 61.1 58.9 Result Š.

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Sequence 561, App	Sequence 103, App.	4887					Sequence 1847, Ap	Sequence 1847. Ap		•	324 A		324	789,	324,	789.	324,	789		667					
US-09-841-132-561	US-10-007-693-103	US-09-815-242-4887	US-09-815-242-10482	US-09-815-242-5574	US-09-815-242-12442	US-09-925-300-1515	US-09-736-457-1847	US-09-902-941-1847	US-09-849-626-1847	US-10-017-754-1847	US-09-736-457-324	US-09-736-457-789	US-09-902-941-324	US-09-902-941-789	US-09-849-626-324	US-09-849-626-789	US-10-017-754-324	US-10-017-754-789	US-09-214-881A-10	US-09-736-457-1667	US-09-902-941-1667	US-09-902-941-1913	US-09-849-626-1667	US-09-849-626-1913	
10	12	10	10	10	10	10	0	σ	σ	6	6	σ	σ	σ	6	0	σ	6	10	6	9	σ	6	6	
394	394	395	395	394	394	479	20	20	20	20	200	200	200	200	200	200	200	200	201	207	207	207	207	207	
58.9	58.9	57.8	57.8	53.3	53.3	50.0	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	46.7	
53	53	25	25	48	48	45	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	
20 21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	. 45	

ALIGNMENTS

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; Sequence 10362, Application US/09815242
patent No. US2002006156941
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
                                                                                        Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.3%;
76.5%;
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Best Local Similarity 76.5%;
Matches 13; Conservative
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Zyskind, Judith W.
                  Forsyth, R. Allyn
Froelich, Jamie M.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KFERTKPGVNIGTIXXV 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Escherichia coli
US-09-845-335-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.3
Best Local Similarity 76.5
Matches 13; Conservative
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: E. COli
US-09-912-020-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-815-242-10362
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LENGTH: 394
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US-09-845-335-6
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                                                                 APPLICANT:
                                              APPLICANT:
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                                                                          GENERAL INFORMATION:

APPLICANT: CLOUGH, BARBARA

APPLICANT: CLOUGH, BARBARA

APPLICANT: WILSON ROBERT

TITLE OF INVENTION: AN EF-TU PROFEIN ENCODED ON THE PLASTID DNA OF THE

TITLE OF INVENTION: BALBARIA AND PROTEIN SYNTHESIS INHIBITORS

TITLE OF INVENTION: BALBARIA BARASITE AND PROTEIN SYNTHESIS INHIBITORS

TITLE OF INVENTION: BALBARIA BARASITE AND PROTEIN SYNTHESIS INHIBITORS

TITLE OF INVENTION: BALBARIA BARASITE AND PROTEIN SYNTHESIS INHIBITORS

TITLE OF INVENTION: BALBARIA BARASITE AND PROTEIN SYNTHESIS INHIBITORS

CURRENT APPLICATION NUMBER: US/09/845,335

CURRENT FILING DATE: EARLIER FILING DATE: 1998-08-26

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PALENTIN VET. 2.1

SEQ ID NO 3

LENGTH: 409
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APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: WILSON, ROBERT
TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYMTHESIS INHIBITORS
TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYMTHESIS INHIBITORS
TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYMTHESIS INHIBITORS
TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
FILE REFERENCE: N68837B GGW PLC DP
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/140,466
PRIOR FILING DATE: BARLIER FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 4
LENGTH: 408
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Pred. No. 0.00083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09845335 Patent No. US20020058266A1
                                                ; Sequence 3, Application US/09845335; Patent No. US20020058266A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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73.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Anacystis nidulans
US-09-845-335-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RAKFERTKPHANIGTIGHV 21
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Best Local Similarity 73.79
Matches 14; Conservative
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Matches 14; Conservative
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US-09-845-335-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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         RESULT 2
US-09-845-335-3
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Sequence 6, Application US/09845335
| Patent No. US20020058266A1
| GENERAL INFORMATION:
| APPLICANT: CLOUGH, BARBARA |
| APPLICANT: CLOUGH, BARBARA |
| APPLICANT: WILSON, ROBERR |
| APPLICANT: WILSON, ROBERR |
| APPLICANT: WILSON, ROBERRA |
| TITLE OF INVENTION: MALARRA PARASITE AND PROTEIN SYNTHESIS INHIBITORS |
| TITLE OF INVENTION: BEFECTIVE AS ANTI-MALARIAL COMPOUNDS |
| FILE REPERBORE: N68837B GGW PAC DP |
| CURRENT APPLICATION NUMBER: US/09/845,335 |
| CURRENT FILING DATE: 2001-12-26 |
| PRIOR PILIOATION NUMBER: ERALIER APPLICATION NUMBER: 09/140,466 |
| PRIOR FILING DATE: ERALIER FILING DATE: 1998-08-26 |
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA. 0010-01
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT FILLING DATE: 2000-01-27
PRIOR PRICATION NUMBER: 09/492,709
PRIOR FILLING DATE: 2000-01-27
PRIOR FILLING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SEQ ID NOS: 485
SEQ ID NO 247
LENGTH: 394
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pred. No. 0.0018;
1; Mismatches 3; Indels
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Pred. No. 0.0018;
1; Mismatches 3; Indels
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-815-242-11059
                                                       SEQ ID NO 10431
LENGTH: 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 40all, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tammoto, Robert T.
APPLICANT: You H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITAN.011a
FILE REPERENCE: ELITAN.011a
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
APPLICANT: Xu, F. Howard
APPLICANT: Xu, F. Howard
APPLICANT: Xu, F. Howard
APPLICANT: Xu, F. Howard
APPLICANT: Xu, H. Proxery
                                                                                                                                                                                 TITLE OF INVENTION: PROKATYOUSES

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR PEDLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PELICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-26

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FEASTSEQ FOR WINDOWS VERSION 4.0
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/205
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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APPLICATION NUMBER: 60/269,308
                                                                                                                                                                     Prokaryotes
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Best Local Similarity 76.5%;
Matches 13; Conservative
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Pred. No. 0.0018;
1; Mismatches 3; Indels
                                                                                                Score 66; DB 10; Length 394;
Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TIMALE, JOHN D.
APPLICANT: Cart. Grant J.
APPLICANT: Cart. Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELIFRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001.03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000.03-21
PRIOR FILING DATE: 2000.05-26
PRIOR FILING DATE: 2000.05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000.10-32
PRIOR PILING DATE: 2000.10-32
PRIOR FILING DATE: 2000.11-27
PRIOR FILING DATE: 2000.11-27
PRIOR FILING DATE: 2000.11-27
PRIOR FILING DATE: 2000.12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLILING DATE: 2000.12-22
PRIOR FILING DATE: 2000.12-22
                                                                                                                                                  1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Haemophilus influenzae US-09-815-242-11059
                                                                                                73.38;
76.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ohlsen, Kari L. APPLICANY: Syskind, Judith W. APPLICANY: Wall, Daniel APPLICANY: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
                                                                                                Query Match 73.37
Best Local Similarity 76.59
Matches 13; Conservative
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; TYPE: PRT; ORGANISM: Escherichia coli
US-09-815-242-10431
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Best Local Similarity 76.5
Matches 13; Conservative
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                   APPLICANT: Xu, H. HOWARD

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SUFFWARE FELSER FEASEER FOR WINDOWS VERSION 4.0
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APPLICANT: Tyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CUBRENT APPLICANTON NUMBER: US/09/815,242
CUBRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELLORICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PILING DATE: 2000-10-23
PRIOR PELLORICATION NUMBER: 60/253, 625
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Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                           Yamamoto, Robert T.
Zyskind, Judith W.
                        Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
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hes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 11069
LENGTH: 394
                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Matches
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Sequence 9, Application US/08831310
Patent No. US20020026035A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold et al.
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.0018;
1; Mismatches 3; Indels
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Pred. No. 0.00037;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASISE for Windows Version 2.0 SOFTWARE: FASISE for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,310 FILING DATE: 01-APR-1997 CLASSIFICATION: 435 ATTORNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06132/037001
TELECHONE: 617-428-0200
TELEFAX: 617-428-0705
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13964
LENGTH: 409
                                                                                                                                                          ; LOCATION: (1)...(409)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-13964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
                                                                                                                                                                                                                                     73.3%;
76.5%;
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76.5%;
                                                                                                                                                                                                                                                                                                                                       20 KFERTKPHVNVGTIGHV 36
                                                                                                 ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                   Query Match 73.3
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                   3 KFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
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Best Local Similarity
                                                                                                                                        NAME/KEY: VARIANT
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COUNTRY: U
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                                                                                 TYPE: PRT
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Score 62; DB 10;
Pred. No. 0.0086;
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Sequence 11995, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                         ; Sequence 11415, Application US/09815242
; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr, Grant J.
Yamamoto, Robert T.
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76.58;
                                                       68.9%;
76.5%;
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KFERTKPGVNIGTIXXV 19
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                                                                                                                                                            Local Similarity 76.5
hes 13; Conservative
                                                     Query Match 68.9
Best Local Similarity 76.5
Matches 13; Conservative
; FRAGMENT TYPE: internal US-08-831-310-4
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                      RESULT 14
US-09-815-242-11415
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APPLICANT:
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Patent No. US20020026035A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Helicobacter GHPO 1360 and
TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                            Sequence 1, Application US/09488737;
Sequence 1, Application US/09488737;
Patent No. US20020151462a1;
GENERAL INFORMATION:
APPLICANT: Lissol. Ling
TITLE OF INVENTION: Helicobacter Pylori Membrane Proteins;
FILE REFERENCE: 50019/005002;
CURRENT APPLICATION NUMBER: US/09/488,737
CURRENT FILING DATE: 2000-01-20
PRIOR FILING DATE: 1998-02-19;
PRIOR FILING DATE: 1998-02-19;
PRIOR FILING DATE: 1996-10-04
PRIOR FILING DATE: 1995-10-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.9%; Score 62; DB 10; Length 22; 76.5%; Pred. No. 0.00037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 4; Indels
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APPLICATION NUMBER: US/08/831,310 FILING DATE: 01-APR-1997
(TGASSIFICATION: 435
VITORNEY AREPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06132/037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-488-737-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KFERTKPGVNIGTIXXV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KFNRTKPHVNIGTIGHV 20
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Matches 13; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                    US-09-488-737-1
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 22
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APPLICANT: Chisen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramamoto, Robert T.
APPLICANT: Tramamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: IDENTICATION NUMBER: US/09/815,242
CURRENT ELLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-02-16
Score 62; DB 8; Length 399;
Pred. No. 0.0086;
0; Mismatches 4; Indels
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Search completed: April 29, 2003, 09:49:33 Job time: 15 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model OM nucleic - nucleic search,

May 1, 2003, 05:55:55 ; Search time 5099 Seconds (without alignments) 9594.394 Million cell updates/sec Run on:

US-09-810-764A-6 1681 Perfect score:

1 atteceaaataateeecaee......gttaaaaaaaaaaaaaaa 1681 Sequence:

2054640 seqs, 14551402878 residues Searched:

IDENTITY_NUC Gapox 1.0

Scoring table:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmb1:* Database

em_ba:* em_fun:* em_hum:* em_in:* gb_ba: *
gb_htg: *
gb_om: *
gb_ow: *
gb_ov: *
gb_pt: *
gb_pl: *
gb_pr: *
gb_ro: * em_pat:* em_sts:* em_un:* em_vi:* gb_sy:* gb_un:* gb_vi:* em_ph:* em_pl:* em_or:* em_mu:* em_om:* em_ro:* Pred. No. is the number of results predicted by chance to have a

em_htgo_mus:*
em_htgo_other:*

em_htgo_hum:*

em_htg_inv:*
em_htg_other:*
em_htg_mus:*

em_htg_pln:* em_htg_rod:* em_htg_mam:* em_htg_vrt:*

em_htg_hum:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES	q.	1	AP00402	AF327	•		AF23453				ATTUFA	AF4	AY07435	ATF9F13	ATC	TOBTUFB		TOBTUFA	L AP005375		0		AP00359	D90913			879408		1 SCTUFIFUS			1 TCHOESTUF				1 AE011727		AE0117	AE00484	SRTUF1	AE0048	AEUUSBU
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	Ş	aroas	215	10	200	790.6	<u>`</u>	Ξ	03	00	87	ວິດ	85	85	85	7.5	75	28	30	אנ	604.4	04	90	ויט	2	553.4	48	48	י רש	539.8	0000	36	36	35	33	532.6	31	3.1	2	201	7 0	7
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ALIGNMENTS

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AP004023 138931 bp DNA linear HTG 21-MAR-2002 Oryza sativa (japonica cultivar-group) chromosome 2 clone 0.31126_D09, *** SEQUENCING IN PROGRESS ***, in ordered pieces. AP004023 DEFINITION ACCESSION

AP004023.1 GI:15130685 HTG; HTGS_PHASE2. VERSION KEYWORDS SOURCE

Oryza satīva (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OJ1126_D09. ORGANISM

Oryza sativa (japonica cultivar-group) Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Enrhartoideae, Oryzeae, Oryza.

REFERENCE

```
combining Monsand and RGF-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence."
                                                                                                                    Direct Submission
Submitted (08-AUG-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibarsui 305-8602, Japan (E-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98476 ACCAAGCCGCACGTCAACATCGGCACCATCGGCCACGTCGACCACGGGAAGACTACGCTG 98535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98296 GCCTCCGCATACACCTGCCTGGTCTTCTCCACCTCCTCCTCCAAGCCGGCTCGGCTCC 98355
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/cultivar="Nipponbare"
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                              * by the finished sequence as soon as it is available
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566 others
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                                                                                                 Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
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0; Mismatches 25
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                                                           Published Only in Database (2001) 2 (bases 1 to 138931)
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98836 CCCAAGATTGTTGTCTTCCTCAACAAGAAGGACCAGGTCGACGAGGAGGTGCTCCAG
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                                                                                                                                                      661 CTCGTCGAGCTCCGCGAGCTGCTCAGCAACTACGAGTACGACGGCGACGACGTA
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                                                                            CCCAAGATCGTTGTCTTCCTCAACAAGAAGGACATGGTCGACGACGAGGAGCTGCTCGAG
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YENGDEVYLVAGSALKALENIMANPAIKRGDDEWYDGIFSLIDSVDDYIPYPPQRQTD
ILPFLLAVEDVFSITGRYNKYGDTEWYNGIRETRNCTYTGVETGYD
DDAMAGDNVGLLLRGMCKDDIERGRYNKYGDTAVTVGIRETRNCTYTGVETGYTF
PGYRPQFYNKTIDVTGNVTKIMNDKDEEARMCMPGDRVYVYLLIQPVACEGGMRFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MASLASASASTSLVFSTSSSKPRLGSSVGFSSPARFRRTAAAAA
SRGTGRRAGLLVVRAARGKFERTKPHVNIGTIGHVDHGKTTLTAALTMVLASVGGSAP
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                                                                                  PLN 02-DEC-2001
                                                                                                                                                                    Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. 1 (bases 1 to 2050) Lee,J.-H. and Kim,J.-K.
                                                                                                                                                                                                                                                                        Direct Submission
Submitted (10-DEC-2000) Korea University, 5-1 Anam-Dong, Seong
Buk-Gu, Seoul, Seoul 136-701, South Korea
Location/Qualifiers
1.2050
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                                                                                          Oryza sativa translational elongation factor Tu (tufA) genecomplete cds; nuclear gene for chloroplast product.
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/protein_id="AAL37431.1"
/db_xref="GI:17225494"
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1621 TATCTGGTTGCAACTCATTTGGCTAAGAGGTGCCATCTACTGTTA 1665
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Pred. No. 2.3e-153;
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/db_xref="taxon:4530"
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SKGTGRRAGLLVWRRAARGKFERTKPHVNIGTIGHVDHGKTTLTAALTMYLASVGGSAP
KKYDEIDAAPEERARGITINTATVEYETETRHYAHVDCPGHADYVKNNITGAAQMDGA
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YEYDGDEVPIVAGSALKALENLMANPAIKRGDDEWVDGIFSLIDSVDNYIPVPQRQTD
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa chloroplast translational elongation factor Tu (tufA) mRNA, complete cds; nuclear gene for chloroplast product.
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Lee, J.H., Lee, J.W., Chung, Y.Y., Paek, K.H., Shin, J.S., Yun, C.H. and
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1321 GGTGACCGTATCAAAATGATTGTTCAGCTCATCCAGCCTGTTGCTTGTGAGCAGGGTATG 1380
                                  1387 GGTGACCGTGTCAAGATGGTTGTGGAGCTCATCCAGCCCGTCGCTTGTGAGCAGGAATG 1446
                                                                        1381 AGGTTTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGCCGGTGTCATCAACAAAATCATT 1440
                                                                                         1561 ACACTTTTTTTTGTCAAGTGAATTTGCATAATTTATGACATTCACGACAAAGATTCACA 1620
                                                                                                                                               1441 GAGTAAACTGGATATAACATATCCACCATGAGAATTTTCCTTGTTTACTCAAAGCGACAT 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Korea University, Seong Buk Gu,
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/cultivar="Japonica Nipponbare"
/db_xref="taxon:39947"
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                                                                                                                             9;
                                                                                                                               Indels
                                                                                   DB 8;
                                                                                                                             Mismatches 259;
                                                                                 Score 1200.6; DB 8
Pred. No. 5.2e-152;
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PEGGKTVGAGVINTILK"
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83.9%;
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                                                                                                                               Matches 1395; Conservative
                      512
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                                                                                     Query Match
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PLN 15-0CT-1997
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-JUL-1995) E. Stutz, Laboratoire de Biochimie,
Universite de Neuchatel, Rue Emile-Argand 11, CH-2007 Neuchatel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1400 AGGTTTGCCATCCCTGAGGGTGGAAAGACCGTCGGTGCCGGCGTCATCAATACGATTTG 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTTTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGCCGGTGTCATCAACAAAATCATT 1440
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                                                                                                                                                                                    1220 CGGCACTCACCGTTTTTCCCTGGTTACCGCCCTCAGTTCTACATGCGGACTACCGATGTG
                                               GTTGAGATGTTCCAGAAGACCATGGATGATGCCATGGCCGGAGACAATGTTGGGCTGCTG
                                                              CTCCGTGGTATGCAGAAGGATGACATTGAAAGAGGCATGGTGCTGGCAAAGCCTGGCTCT
                                                                                                                         GGTGACCGTATCAAAATGATTGTTCAGCTCATCCAGCCTGTTGCTTGTGAGCAGGGTATG
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                                                                                                                                                                                                                                 CGACACTCACCTTTCTTCCTGGTTACCGCCCACAGTTCTACATGCGGACAACTGATGTG
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The tuf gene family of soybean: structure and differential
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G.max DNA for EF-Tu chloroplast specific protein.
X89058
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AUTHORS
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NMITGAAQMDGAILVVSGADGPMPQTKEHILLAKQVGVPNIVVFLNKQDQVDDEELLQ
LVELEVRELLSKYEFPGDDVPIISGSALLSLEALMANPSIKRGENQWYDKIYELMEAV
DDYIPIPQRQTELPFLLAIEDVFTITGRGTVATGRVERGFIRVGETVDIVGVKDTRNT
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KKEEGGRHSPFFSGYRPQFYMRTTDVTGKVTEIMNDKDEESKMVMPGDRVKLVVELIV
                                                                                                                                                                                                                                                                                               /db_xref="SWISS-PROT:P46280"
/translation="MAISWAAATTSKLAYPPHVHFSPSPSSNYLFLKTHKPSATHLSS
                                                                                                                                                                                                                                                                                                                                  SFIHPTIILHLAAANTTTRRRSFTVRAARGKFERKKPHVNIGTIGHVDHGKTTLTAAL
TWALASLGNSAPKKYDEIDAAPEERARGITINTATVEY ETENRHYAHVDCPGHADYVK
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                                                                                                                                                                                                          /note="chloroplast specific"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 891
                                                                                                                                                                                                                                            /product="EF-Tu protein"
                                                                                                                                                                                                                                                       /protein_id="CAA61444.1"
/db_xref="GI:949873"
                                                                                                                    /evidence-experimental
1219. .2658
/gene="tufB1"
1219. .2658
/gene="tufB1"
                /organism="Glycine max"
/cultivar="Ceresia"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
712 c 646 g
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2922
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1142. .>2658
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/gene="tufB1"
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/gene="tufB1"
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PLN 25-JUL-1996
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                  2005 AACCAATGGGTTGATAAAATTTACGAGCTCATGGAAGGTGTGGATGACTACCATC 2064
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                                                                        ACTACGATTATGAATGACAAGGATGAGGAGGCGAAGATGTGCATGCCTGGTGACCGTATC 1332
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Submitted (17-MAY-1992) E. Stutz, Lab. de Biochimie Vegetale,
Universite'de Neuchatel, Chantemerle 18, CH-2000 Neuchatel,
SWITZERLAND
                                                                                                                                                                                                                                                   GAGGTCCGCGAGCTGCTCAGCAACTACGAGTACGACGGCGACGACGTACCAATCGTCGCCT
                                                         GGCTCCGCCCTCAAGGCGCTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGGGAC
                                                                                                                 GATGAGTGGGTCGACTACATCTTCTCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTC
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/translation="MAVSSATASSKLILLPHASSSSSLNSTPPRSSTTNTHKLTPLSS
SFLHPTTVLRRTPSSTTTPRRTFTVRAARGKFERKKPHVNIGTIGHVDHGKTTLTAAL
TMALAALGNSAPKKYDEIDAAPEERARGITINTATVEYETENRHYAHVDCPGHADYVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMITGAAQMDGAILVVSGADGPMPQTKEHIILAKQVGVPNMVVFLNKQDQVDDEELLQ
LVEIEVRDLLSSYEFPGDDTPIVSGSALLALEALMANPAIKRGDNEWVDKIFQLMDEV
DNYIPIPQRQTDLPFLLAVEDVFSITGRGTVATGRVERGTIKVGETVDLVGLRETRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVTGVEMFOR I LDEALAGDNVGLLLRGVOKTDTORGMTLAKPOTTTPHTKFSALVYVL
KKEEGGRHSPFFAGYRPQFYMRTTDVTGKVTSIMNDKDEESTMVLPGDRVKMVVELIV
PVACEQGMRFAIREGGKTVGAGVIQSIIE"
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2 (bases 1 to 2313)
Bonny,C. and Stutz,E. Soybean (glycine max 1.) nuclear DNA contains four tuf genes conding for the chloroplast specific translation elongation factor
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                                                                                                                                                                               /tissue_type="leaves"
/clone_lib="genomic dna"
220. .253
/note="light responsive element"
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Pred. No. 1.5e-96)
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/db_xref="GI:18776"
                                                                                                                                              /cultivar="Maple Arrow"
/db_xref="taxon:3847"
                                                                                                   Location/Qualifiers
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                                                                                Chimia 47, 247-249 (1993)
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/gene="tufA"
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923. .2146
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/gene="tufA"
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710. .2149
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AUTHORS
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                                      1336 TCTCCGGCCGACGGCCCCATGCCCCAAACCAAAGAACACATAATATAGCGAAACAAG
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                        473 CCGACTATGTCAAGAATATGATCACCGGCGCTGCGCAGATGGACGGTGCCATCCTCGTCG
                                                                         TCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAGGACATGGTCGACGACGAGGAGC
                                                                                                                                                                            TGCTCGAGCTCGAGCTCGAGGTCCGCGAGCTGCTCAGCAACTACGAGTACGACGGCG
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                                                                                                                                                                                                                                                                            TGGATTCCTATATTCCAGTCCCGCAGAGGCAGACTGACCTCCCGTTCTTGCTCGCTGTTG
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Signsapkkydeidaapeeragitinyatveyetenhyahvdcpghadyvknwitg
Aaqwigailvyvsgadspmpoffkehillakvyveypunwyyelnkodyddeelleelvele
VRELLSAYEFPGDEVPIISGSALLALEALMANPAIKRGENWWDKIFSLMDSVDSYIP
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EMFORTLDEALAGDNVGLLLRGVQKEDITRGMVLAKPGTITPHTKFSAIVYVLKKEEG
GRHSPFFAGYRPQFFVRTTDVTGKVATIMNDKDEESKMVMPGDRVKMVVELILPIACE
ARNA linear PLN 15-FEB-2001
Pelargonium graveolens chloroplast translational elongation factor
Tu (tufA) mRNA, complete cds; nuclear gene for chloroplast product.
AF234537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="chloroplast translational elongation factor/protein_id="AAK08141.1"
/db_xref="GI:12830555"
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                                                                                                                                                                                                                                                     1 (bases 1 to 1584)
Kang,C.J., Lee,M.G., Cho,Y.S., Lee,J.W., Kyung,Y.J., Shin,J.S.
Kim,E.S. and Kim,J.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee, J.W., Kyung, Y.J., Shin, J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-FEB-2000) Biology, Korea University, Seong Buk
                                                                                                                                                                Pelargonium graveolens
Marayota, Viridiplantae, Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; Geraniales; Geraniaceae; Pelargonium.
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/db_xref="taxon:73200"
1. .1584
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438 c 396 g 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 5-1, Seoul, Korea
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                 AF234537.1 GI:12830554
                                                                                                                                               Pelargonium graveolens.
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1584)
Kang, C.J., Lee, M.G., C
Kim, E.S. and Kim, J.K.
Direct Submission
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PSY14561 1731 bp mRNA linear PLN 26-OCT-1999
Pisum Sativum mRNA for choloroplast translation elongation factor.
Y14561
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Direct Submission
Submitted (InI-NG-1997) M.K. Reddy, International Centre for Submitted (InI-NG-1997) M.K. Reddy, International Centre for Submitted (InI-NG-1997) M.K. Reddy, International Centre for Submitted (InI-NG-1997) M.K. Reddy, International Biology Lab, Aruna Asaf Ali Marg, New Delhi - 110 067, INDIA
Location/Qualifiers
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Plant Mol. Biol. 41 (1), 125-137 (1999)
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GCHADYVKNNITGAAQMOGAILWSGAADGPHQTKEHILLAKQVGYPSYVYFLNKOO
QVDDEELLELVELEVRELELSKYEFPGDDIPIVSGASALLALLEALMANPTKRKGNOWVD
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VGLRETRNTTYTGVEWFQKILDDAMAGDNVGLLLRGIQKIDIQRGWVLAKPGTITPHS
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TLTRLSSSFLNPSTILHLTPSQRTNRPSSSPFTVRAARGKFERKKPHLNIGTIGHVDH
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/db_xref="taxon:3888"
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1 (bases 1 to 2342)

10 (Susin, V.W., Becker, C.K. and Shewmaker, C.K.

Cloning and nucleotida sequence of a tobacco chloroplast translational elongation factor, EF-Tu
Plant Physiol. 101 (1), 333-334 (1993)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="translation elongation factor EF-Tu"
/protein_id="AAA18546.1"
/db_xref="GI:170344"
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to nascent polypeptide during translation"
/codon_start=1
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                                       linear
                                                                                                                                 chloroplast translation elongation factor EF-Tu.
Nicotiana tabacum (variety NK236) DNA.
Nicotiana tabacum
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Pred. No. 2.7e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4097"
/clone_lib="lambda EMBL3 genomic"
344. .1780
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Nicotiana tabacum'
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72.0%;
                                                                                                           M94204.1 GI:170343
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                                                                                                                                                       1007 GAGGTAAGAGAGTTATGTCAAGTTATGAGTTTCCTGGTGATGATATTCCTATTATTTCT 1066
                                                                                                                                                                                                         1067 GGCTCTGCTCTTTGGCTTTTAGAGGCTTTGATGGCTAATCCTAGTATTAAGAGGAGGTGAA 1126
                                                                                                                                                                                                                                                    973 GTCGATATCGTCGGAATCCGGGACACCCGGAACTGCACGGTCACTGGTGTTGAGATGTTC 1032
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 GTCTTCCTCAACAAGAAGGACATGGTCGACGAGGAGGTGCTCGAGCTCGTCGAGCTC
                                                                                                                                                                                 733 GGCTCCGCCCTCAAGGCGCTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGGCAC
                                                                                                                                                                                                                                   793 GATGAGTGGGTCGACTACATCTTCTCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTC
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PLN 01-FEB-2000

2667 bp DNA linear PLN 01-FEB-20 Nicotiana sylvestris tufA gene for chloroplast elongation factor D11469

DEFINITION

ACCESSION

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Sugiura,M.
Sugiura,M.
Direct Submission
Direct Submission
Submitted (19-JUN-1992) Masahiro Sugiura, Nagoya University, Center for Gene Research (Tel:052-789-3081, Fax:052-789-3081)
Location/Qualifiers
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                                                                                                                                                                            Tracheophyta;
                            G-binding protein; elongation factor; nuclear-encoded chloroplast elongation factor TuA(EF-TuA).
Nicotiana sylvestris DNA, clone_lib:lambda Dash.
Nicotiana sylvestris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="chloroplast elongation factor TuA(EF-TuA)"
/protein_id="BAA02027.1"
/db_xref="GI:459239"
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                                                                                                                                                             Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana. I (bases I to 2667)
Sugita,M., Murayama,Y. and Sugiura,M. Structure and differential expression of two distinct genes encoding the chloroplast elongation factor Tu in tobacco curr. Genet. 25 (2), 164-168 (1994)
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/db_xref="taxon:4096"
/clone_lib="lambda Dash"
257. .265
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551
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/gene="tufA"
878. 210.
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668. .2104
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/gene="tufA"
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ilarity 71.9%;
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1 (bases 1 to 2272)
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Evolutionary transfer of the chloroplast tufA gene
Nature 344 (6263), 262-265 (1990)
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/protein_id="CAA36498.1"
/db_xreff="GI:22565"
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/db_xref="taxon:3702"
/clone_lib="Lambda"
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Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jiang, P. X., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamada, K., Yamanura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.
Direct Submission
Submitted (14-SEP-2001) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1663)

Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carinforl, P., Dale, J. M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P. X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nauyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Arabidopsis, CDNA clones
Unpublished
(Dases 1 to 1663)
                                                                         PLN 15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="WAISAPAACSSSSRILCSYSSPSPSLCPAISTSGKLKTLTLSSSFLEPSYSLTTTSASQSTRRSFTVRAARGKFERKKPHVNIGTIGHVDHGKTTLTAALTMALASIGSSVAKKYDEIDAAPEERARGITINTATVEYETERRHYAHVDCPGHADYVKNMI
                                                                                                                                                                                                           FLI_CDNA.
Arabidopsis thaliana.
Arabidopsis thaliana.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                       1663 bp mRNA linear PLN 15-
Arabidopsis thaliana AT4g20360/F9F13_10 mRNA, complete cds.
AF419609
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/db_xref="taxon:3702"
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/db_xref="GI:16930511"
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LEVRELLSSYEFNGDDIPIISGSALLAVETLTENPKVKRGDNKWVDKIYELMDAVDDY
IPIPQRQTELPFLLAVEDVFSITGRGTVATGRVERGTVKVGETVDLVGLRETRSYTVT
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EGGRHSPFFAGYRPQFYMRTTDVTGKVTKIMNDKDEESKMVMPGDRVKIVVELIVPVA
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Chouk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J. M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jiang, P. X., Jones, T., Kamila, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J. M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Arabidopsis, CDNA clones
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Greuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Ishida,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Mitanda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
Davis,R.W., Theologis,A. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing and annotation of the RAFL cDNAS: Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
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AGAGGCATGGTGCTGGCAAAGCCTGGCTCTATCACACGCACACCAAAGTTTGAGGCTGTT 1170
                          1222 ATCTATGTGTTGAAGAAGAAGGAGGTGGAAGGCATTCTCCCATTCTTTGCAGGGTACAGG 1281
                                                                                                                                                                                                                                                                                    1282 CCTCAGTTCTACATGAGGACGACTGATGTTACGGGTAAAGTGACGAAGATCATGAACGAC 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1402 ATTGTGCCGGTGGCTTGTGAACAAGGGATGAGGTTTGCTATCAGAGAAGGAGGAAAGACT 1461
                                                                                                              GTGTATGTGCTTAAGAAGGAAGAGGGTGGCCGACACTCACCTTTCTTCCCTGGTTACCGC
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Arabidopsis thaliana.
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JOURNAL
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GVENFOKILDEALAGDNVGLLLRGIOKADIORGMVLAKPGSITPHTKREAIIYVLKKE
EGGRHSPFFAGYRPOFYMRTTDVTGKVTKIMNDKDEESKMVMPGDRVKIVVELIVPVA
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LEVRELLSSYEFNGDDIPIISGSALLAVETLTENPKVKRGDNKWVDKIYELMDAVDDY
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                                                                               Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                    /note="translation elongation factor EF-Tu precursor,
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Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A. Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.
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Pred. No. 6.8e-83;
0; Mismatches 344;
                                                                                                                                                                     /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                     /clone="RAFL06-16-G16(R13435)"
                                                                                                                                                                                                                                                                                                                                      /product="AT4g20360/F9F13_10"
/protein_id="AAK95315.1"
/db_xref="G1:15294276"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      991 CGGGACACCCGGAACTGCACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGATGAT 1050
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                                                                                          751 CTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTAC 810
800 GITGAGACICITACTGAGAATCCTAAGGTTAAGAGGGGTGATAACAAATGGGTAGATAAG 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LASIGSSVAKKYDEIDAAPEERAKGITINTATVEYETENRHYAHVDCPGHADYVKNMI
TGAAQMDGAILVVSGADGPMPQTKEHILLAKQVGVPDMVVFLNKEDQVDDAELLELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equally to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLPSYSLTTTSASQSTRRSFTVRAARGKFERKKPHVNIGTIGHVDHGKTTLTAALTMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MAISAPAACSSSRILCSYSSPSDSLCPAISTSGKLKTLTLSSS
                                                                                                                                                                                                                                        Submitted (11-7AN-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurali,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                         Yamada.K., Banh.J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
Dang,C.C., Toriuni,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.
Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Yamada,K., Banh,J., Chan,M.M., Chang,E., Dale,J.M., Deng,J.M., Deng,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Meyers,M.C., Miranda,M., Nguyen,M., Pallm,C., Lam,B., Lin,J., Southwick,A., Davis,R.W., Reker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=experimental
/product="putative translation elongation factor EF-Tu
precursor, chloroplast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="This clone is in a modified pBluescript vector (FLC-1) as a BamHI/XhoI insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 1688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
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/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 685.6; DB 8 Pred. No. 6.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RAFL09-55-K09 (R19264)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEQGMRFAIREGGKTVGAGVIGTILE"
Arabidopsis Full Length cDNA Clones
Unpublished
2 (bases 1 to 1688)
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/replace="t"
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/gene="At4g20360"
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72.2%;
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Best Local Similarity
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  TITLE
JOURNAL
REFERENCE
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                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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GCCATGGCCGGAGACAATGTTGGGCTGCTGCTCCGTGGTATGCAGAGGATGACATTGAA 1110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGACACCCGGGAACTGCACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGATGAT 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTTAGCTGGTGACAATGTAGGGTTGTTGCTTAGGGGTATTCAAAAGGCTGATATTCAG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGGIATGGITTTAGCTAAGCCGGGATCGATTACTCCACATACCAAGTTTGAAGCAATT 1239
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211 GTGCGCGCGGCGAGGGGCAAGTTCGAGCGCACCAAACCACGTCAACATAGGCACCATC 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 871 CICCCGIICIIGCICGCIGIIGAAGAIGICIICICCAICACCGGICGIGGIACAGIIGCC 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 TIGCCATICTIGITAGCIGITIGAGGAIGTGTTCTCIAICACTGGACGTGGACGGIGGCT 999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             820 GTTGAGACTCTTACTGAGAATCCTAAGGTTAAGAGGGGGTGATAACAAATGGGTAGATAAG
                                                                                                                                                                                                                                                                                                                                                                               631 GACATGGTCGACGAGGAGGAGCTGCTCGAGCTCGAGGTCGAGGTCCGCGAGCTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   751 CTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTAC
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                                                                                                                271 GGCCATGTCGACCACGGAAAGACCACTCTCACCGCCGCGCGCTCACCATGGTGCTCGCCTCC
                                                                                                                                              331 GTCGGTGGCAGCGCGCCTAAGAAGTACGACGAGATCGACGCCCCCCGAGGAGCGCGCC
                                                                                                                                                                                                                                                                                       400 ATTGGTTCCAGCGTCGCTAAAAAGTACGACGAGATTGACGCTGCGCCGGAGGAGAGCT
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                                                      280 GICCGCGCCGCTCGTGGAAAGTTCGAGAAGAAGAAGCCTCATGTCAACATCGGAACCATC
                                                                                                                                                                                                                                                                                                                                              CGCGGTATCACCATCAACACCGCCACCGTCGAGTACGAGACCGAGACCCGCCACTACGCA
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DVEKELLKIGLKPATNTAERRAAAQTHGISNKPKDKKKKKQEISKRTKLTNAHLPELF
                                                                                                                                                                                                                                                                            .2299)
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                                                                                                                                                                                                                                                                                                                                                                                               .2637)
                                  complement(1281, .1631)
                                                                                                                                                         .2075)
                                                                                                                                                                                                                   .2167)
                                                                                                                                                       complement(1959.
/gene="F9F13.2"
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/gene="F9F13.2"
                                                                                                complement(1632.
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3903. .4022
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3665. .3782
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                                                                                                                                                                                                                                                                                                               ATF9F13 109936 bp DNA linear PLN 16-AUG-1999
Arblidopsis thaliana DNA chromosome 4, BAC clone F9F13 (ESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing, project.

BU Arabidopsis sequencing, project.

Direct Submission

Binchemie, Am Klopferspitz 18a, D-83152 Martinsried, FRG, E-mail:

Schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael.bevan@bbsrc.ac.uk

on May 18, 1999 this sequence version replaced gi:526218B.

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MALKEQLDKFNKQQVKCQSTLSSIASSRERTSSSRQNVPLPAAI
TYQKRDAAAVVKRSSDTERLOQINNNIRTAAPVGAQIRTVTDLLEVERLALITPEQINEWCH
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AYPNVMEDLRALSASGDIYLLSNSQEDIAYPUDFKCEIKVDDEFKALFRDINIPNDML
                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="EST GB:233733 marks last intron
EST GB:146736 marks 5' non-coding exon
weak similarity to TRANSCRIPTION INITIATION FACTOR IIE,
BETA SUBUNIT - XENOPUS LAEVIS, SWALL:TZEE_XENLA
contains EST gb:144730;233733;146736"
                                1291 AAGGATGAGGAGGCGAAGATGTGCATGCCTGGTGACCGTATCAAAATGATTGTTCAGCTC 1350
                                                                                          1351 ATCCAGCCTGTTGCTTGTGAGCAGGGTATGAGGTTTGCTATCCGTGAGGGTGGTAAGACC 1410
                                                                                                                complement(join(1281. .1631,1959. .2075,2168. .2299, 2377. .2637))
/gene="F9F13.2"
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Bevan,M., Pohl,T., Weizenegger,T., Bancroft,I., Mewes,H.W., Mayer,K.F.X., Lemcke,K. and Schueller,C.
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                                                                                                                                                                    1411 GTTGGTGCCGGTGTCATCAACAAAATCATTGAGTAA 1446
                                                                                                                                                                                          /product="putative protein"
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/db_xref="taxon:3702"
/chromosome="4"
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/gene="F9F13.2"
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4561. 4670,4763. 5173,5213. 5372,5484. 5669,5813. 6017,
6246. 6346)
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RAKMYSYAVGGTPGRAEDNYKFHTHSYCCLDYAOTYDIVRYKLHRLKKRFRDELEDR
NTVQEYGCPNCKRYNALDALRLISMEDDSFHCENCNGELVBRGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARRROREKVKVWLQDLEVCVYCFSGYFNESMRKTQIDLPSLKLVHRSKFMMKSERYMI
KFPRRFILKYPWLETCKTKGDCGCSVCVDTJGNKIVKDLPFPAFEPFPAWEARAARA
RENGDFNDDDSRSLGGYGSTPMPFLGETKVEVNLGEGNEDVTSTGGDSSLKMLPPWM
IKGGNKLTEEGRGEMRQEANVGEBAKLSDDKKSDEYLKAYAAIMEQOKLAAKINEQ
ESAGESTTTDIESARTYSDRQVGMKSKREEEEEDVEWEEGASVAANGNYKVDLNVEAE
EAEEKEDGDEDDDIDWEEG"
                                                                                                                                                                   /note="weak similarity to transcription factor IIE alpha-Xenopus laevis, PIR2:S26646"
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Matches 892; Conservative 0; Mismatches 344; Indels 0; Ga 211 GTGCGCGCGCGGGGGGGCAAGTTCGAGCACCAAACAACAACAACAACAACAACAACAACAACA	Db 8949 ATTGGTTCCAGCGTCGCTAAAAAGTACGACGAGTTGACGCTGCGCGGAGAGAGA	Db 9069 CAGTTGATTGTCTGTTTTTTTTTTTTTTTTTTTTTTTTT	OY 571 CACATCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAAGAAG 630	691 AGCAACTACGACGACGACGACCTACCAATCGTCGCTGGCTCCGCCCTCAAGGCG	OY 811 ATCITCTGTIGGTGGATGGATTCCTATATTCCAGTGCGGAGGGGGGGGGG	QY 931 ACTGGCCGTATAGAGCGTGGCACCGTCAAGATTGGTGACACAGTCGATATCGTCGGAATC 990	QY 1051 GCCATGGCGGAGAAATGTTGGGCTGCTGCTGCTATGCAGAAGGATGACATTGAA 1110	
4 4 4 4	/gene="F9F13.4" //number=7 exon :54845669 /gene="F9F13.4" /number=8 intron 56705812 /gene="F9F13.4"	exon 58136017 /gene="F9F13.4" /number=9 intron 60186245 /gene="F9F13.4"	exon 62466346 /gene="F9F13.4" /number=10 gene 69898331 /gene="F9F13.6" CDS join (69897084,71627222,73167354,74547566, 77037925,80338079,81858331)	/gene="19913.6" /note="similarity to hypothetical protein - Caenorhabditis /note="similarity to hypothetical protein - Caenorhabditis elegans, SPTREMBL:Q17527" /codon_start=1 /product="putative protein" /protein_id="cae52823.1" /db_xref="G1:5738380" /translation="MELERFRVGLTPTVFYIPGFITDEEQTQLLNHIYGASGSKWTL KNRRQNWGRWGLYPQELPPWITXITATARIHESSGLFFSAINHULINEYHDDGI MPHORGDAYPRVATISICSGPRVAMETERINGSFORDER	MINIORATE TVALLES TVALLES TO TELLARISED TELLARISES TO TELL		no	intron 75577037925 exon 77037925 Ouery Match 40.8%; Score 685.6; DB 8; Length 109936; Best Local Similarity 72.2%; Pred. No. 4e-83;

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ATCHRIV52 198427 bp DNA linear PLN 16-MAR-2000 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
Arabidopsis thaliana
Bubraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission State of the Max-Planck-Institut fuer Submission Submitted (10-Max-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
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Schistrosoma mansconi, PATCHX:6454844
contains BST gb.A1994604.1, R30520, A1992766.1, T20423,
AA712864, H76323"
                                                                                                                                                           9969 ATTGTGCCGGTGGCTTGTGAACAAGGGATGAGGTTTGCTATCAGAGAAGGAGGAAGAAT 10028
1291 AAGGATGAGGAGGCGAAGATGTGCATGCCTGGTGACCGTATCAAAATGATTGTTCAGCTC 1350
                            1351 ATCCAGCCTGTTGCTTGTGAGCAGGGTATGAGGTTTGCTATCCGTGAGGGTGGTAAGACC 1410
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1,T., Weizenegger,T., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
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Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Mewes,H.W.,
LemcKe,K. and Mayer,K.F.X.
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                                                                                                                                                                                                                                                                   10029 GTTGGTGCTGGAGTTATTGGGACGATCCTCGAATGA 10064
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join(7547. .8329,8375. .8512)
/gene="AT4_919950"
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Unpublished
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EU Arabidopsis sequencing, project.
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.12332,
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YSLLIPLITENTPOMREDBLTTYSRT
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TVASLYTGKPVSFSSTWSAIPLVLKRLFITFLWVSLLMLAYNTVFLIFLVTLIVAVDL
                                                                                                                                                                     QNVVIAVFSLVVIFVLFLVVHVXMTALMHLASVVSVLEPIYGLAAMKKSYELLKGKTL
MACSMVFIYLVHCGFIAGVFGAVVVRGGDDYGIFARIVAGGFLSVFYYVCKSFHHQEI
DKSALHDHLGGYLGEYVPLKSNIQMENFEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similarity to putative potassium transporter AtKT2p & AtKT1p, Arabidopsis thaliana, Patchx:G2384669 & Patchx:G2384671
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LSSFIRIETMMEPTSNSSTYSSYVSVNHTQDSTVDLIHNNNNHNHNNNMDMFSSMVDY
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12383. 12643,12687. 12887,12986. 13288,13407. 13929,
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/codon_start=1
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join(15812, .16087,16379, .16756,17694. .18160,21289. .21472,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thaliana, PATCHX:E32696 and gamma 'Greek key' motif signature AA308-323;crystallins beta and gamma 'Greek key' motif signature AA47-662;Prokaryotic membrane lipoprotein lipid attachment site AA47-57;Prokaryotic membrane lipoprotein lipid attachment site AA47-57;Prokaryotic membrane contains EST gb:A1993954.1, T42200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIVLLVTTVTLSCLLFFKSANNPLNMVFSPWKTDCYASKLTNESSSKTEPKKEPVSEL
ERVLMNAAMEDNTVIITALNQAWAEPNSTFDVFRESFKVGIETERLLKHVIAVCLDIK
AYDQCLKVHPHCYLINATDSDQLSGPNRFMTPGYLKLIWRRNDLLRQVIGGINFFT
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IRSSRKFPGKHDQDVFNFIKNDLHVEKLGIKMRFFDTVYFGGFCQPSRDINVVNTMHA
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LVLGLAACLLLYKTAYPLHQELDVNNLSSRPLLDHTSSSSPLTRSKSISFREVLENAS
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HPNCYYLKTTGTDFSGEKLFATPDYLKMMWRRIELLTQVLEMGYNFIFTDADIMMLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPRLYPDGDFOMACDRFFGDPHDSDNWVNGGFTYVKSNHRSIBFYKFWYNSRLDYPK
MHDQDVFNQIKHKALVSEIGIQMRFFDTVYFGGFCQTSRDINLVCTMHANCCVGLAKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="similarity to predicted protein, Arabidopsis
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Length 198427;

DB 8;

40.8%; Score 685.6; DB 8 72.2%; Pred. No. 3.7e-83;

Best Local Similarity

Query Match

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DD 188283 TCGTCTTATGAATTTAACGGTGATGATGATCCGATTATCTCTGGTTCTGCTCTTTAGCC 188342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 188463 ITGCCATTCTTGTTAGCTGTTGAGGATGTGTTCTCTATCACTGGACGTGGTGGTGGGT 188522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 188523 ACAGGGCGTGTCGACAGAGGTACGGTTAAGGTAGGAGAGACTGTAGATTTAGTGGGTTTG 188582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 188583 AGGGAGACTAGGAGTTACACTGTCACTGGGGTTGAAATGTTTCAGAAGATTCTTGATGAG 188642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 188223 GATCAAGTAGATGATGCAGAGTTGCTAGAGCTCGTTGAGCTTCGTGAGCTTCTC 188282
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                                                                                              DD 187803 GTCCGCGCCGCTCGTGGAAGTTCGAGAAGAAGCCTCATGTCAACATCGGAACCATC:187862
                                                                                                                                                                                                                               DD 187863 GGTCATGTTGACCATGGGAAAACTACTTTAACCGCAGCTCTAACCATGGCTCTGGCTTCC 187922
                                                                                                                                                                                                                                                                                                                                                                           DD 187923 ATTGGTTCCAGCGTCGCTAAAAGTACGACGAGATTGACGCTGCGCCGGAGGAGAGAGT 187982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DD 188043 CACGTTGATTGTCCTGGTCACGCTGATTACGTTAAGAATATGCATAACGAAGCTGCACAG 188102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 751 CTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTAC 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  811 ATCTTCTCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTCCCGCAGAGGCAGACTGAC 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                871 CICCCGIICIIGGICGCIGIIGAAGAIGICIICTCCAICACGGICGIGGIACAGIIGCC 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 CACGICGACIGCCCCGGCCACGCCGACIAIGICAAGAATAIGAICACCGGCGCIGCGCAG 510
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                                                                                                                                                                                         271 GGCCATGTCGACCACGGAAAGACCACTCTCACCGCCGCGCTCACCATGGTGCTCGCCTCC 330
                                                                                                                                                                                                                                                                                                                       331 GTCGGTGGCAGCGCGCCTAAGAAGTACGACGAGATCGACGCCGCCGCCGGAGGAGGGGCGCCC 390
                                                       211 GIGCGCGCGCGAGGGCAAGTICGAGCGCACCAAACCACACGICAACAIAGGCACCAIC 270
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0; Mismatches 344; Indels
      Matches 892; Conservative
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Search completed: May 1, 2003, 09:37:37 Job time : 5544 secs

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May 1, 2003, 15:58:03; Search time 480 Seconds (without alignments) 7886.686 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score		% Query Match Length DB	DB	ΩI	Description
1	1405.4	;	i	:		Zea mays DNA fragm
7	687.2			21		Arabidopsis thalia
(1)	685.6			21	AAC51055	Arabidopsis thalia
4	528.4			23	AAS54260	Pseudomonas aerugi
. ro	527.8			13	AAQ20215	Sequence of tufl of
9	526.2			13	AAQ20219	Sequence of Srtuff
7	526.2			13	AAQ20218	Sequence of Srtuff
· 00	524.6	31.2	1194		AAQ20220	Sequence of Srtuf
σ	524			23		Propionibacterium

E 6 6 1 5 8 8 8 8

		E. coli proliferat	Escherichia coli n	E. coli DNA for ce	Salmonella typhi D	E. coli DNA for ce	Bordetella pertuss	Sequence of tuf2 g	Mycobacterium tube	Klebsiella oxytoca	Mycobacterium tube	N. meningitidis pa	Neisseria meningit	N. meningitidis B	N. meningitidis pa	Obesumpacterium pr	Buttiauxella agres	C glutamicum codin	Corynebacterium gl	Elongation factor	C glutamicum codin	Plesiomonas shigel	Helicobacter pylor	Helicobacter pylor	Genomic fragment #	Budvicia aquatica	Proteus mirabilis	Haemophilus influe	Haemophilus influe	Haemophilus influe	Haemophilus influe	Sequence of tuf3 g	Bacillus lichenito	Shewanella putrefa	Staphylococcus epi	
AAS54267	AAQ20221	AAA65894	AAH00707	AAS52628	AAS56229	AAS52697	AAH00872	AAQ20216	AA199682	AAH01846	AA199683	AAA81502	AAF21544	AAA81490	AAA81530	AAH01849	AAH01845	AAH68525	AAH00677	AAT92619	AAH68402	AAH01847	AAS53681	AAV07964	AAF28541	AAH01850	AAH01533	AAS53325				Æ		AAH01848	ABN93077	
23	13	21	22	23	23	23	22	13	22	22	22	21	21	21	21	22	22	22	22	18	22	22	23	19	22	22	22	23	23	17	17	13	24	22	24	1
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521.6	518.2	508.8	508.8	508.8	505	503.6	. ~	490	488.4	84	77	472	472	472	462	460.6	455.8	450.2	449.4	446.6	446.4	43	. 4	436	433.4	43	421.8	420.4	420.4	420.4	420.4		413.8	405.4	402 A	
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ALIGNMENTS

AAC46577 standard; DNA; 1657 BP.

RESULT 1

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                   Zea mays DNA fragment SEQ ID NO: 50647.
                                                                                                                                                                          990S-0121825.
990S-0123180.
990S-0123548.
990S-0125788.
99US-0126264.
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99US-0128234.
99US-0128714.
99US-0129845.
                                                                                                                                                       25-FEB-2000; 2000EP-0301439.
                 18-OCT-2000 (first entry)
                                                                                               Zea mays subsp. mays.
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06-APR-1999;
08-APR-1999;
16-APR-1999;
                                                                                                                   EP1033405-A2
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05-MAR-1999;
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23-MAR-1999;
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	14 - MAY - 1999; 18 - MAY - 1999; 19 - MAY - 1999; 20 - MAY - 1999; 21 - MAY - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 28 - MAY - 1999; 29 - JUN - 1999; 04 - JUN - 1999; 10 - JUN - 1999; 10 - JUN - 1999; 16 - JUN - 1999; 16 - JUN - 1999; 16 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 17 - JUN - 1999;		
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990S-0144352.
990S-0144844.
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990S-0145086.
990S-0145088.
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990S-0144972.
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990S-0144973.
990S-0144973.
990S-0144973.
990S-0144973.
990S-014930.
990S-015108.
990S-015108. 14-OCT-1999;

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Pred. No. 1.9e-285;
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                                                             99US-0160814.
99US-0160815.
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14 - OCT - 1999;
14 - OCT - 1999;
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Matches 1505;
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   ATGGACGGTGCCATCCTCGTCGTATCCGGTGCCGACGGCCCCATGCCGCAGACCAAAGAG 570
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                       TCGTCTTATGAATTTAACGGTGATGATATTCCGATTATCTCTGGTTCTGCTCTTTTAGCC
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72.2%; Pred. No. 2.2e-134;
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Matches 892; Conservative
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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Pseudomonas aeruginosa DNA for cellular proliferation protein #391
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                             Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                        Pseudomonas aeruginosa
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es 813; Conserv
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                       181 ATCACCATCAACACCTCGCACGTTGAATACGATTCCGCTGTTCGTCACTACGCCCACGTT 240
                                                                                         420
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                                                                    GACTGCCCCGGCCACGCCGACTATGTCAAGAATATGATCACCGGCGCTGCGCAGATGGAC
  1417 GCCGGTGTCATCAACAAATCATTGAGTAA 1446
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AAQ20219 standard; DNA; 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Substitution of residue 378 of the elongation factor (EF-Tu) with a
                                                                              Sequence of tufl gene encoding translation elongation factor Tul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch al Similarity 67.2%; Pred. No. 2.6e-101; B33; Conservative 0; Mismatches 352; Indels 54;
                                                                                                                                                                                                                                                                                                                                                    PW;
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                                                                                                      Elfamycin resistant actinomycetes; antibiotic resistant;
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                                                                                                                                                                                                                                                                                                                                                    Luiten RGM, Kerkman R, Bosch L, Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                                                                                                        transform streptomycetes to resistant pheno-type
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                                                                                                                                                                   Location/Qualifiers
          AAQ20215 standard; DNA; 1194 BP
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                                                         (first entry)
                                                                                                                                           Streptomyces ramocissimus
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                                                                                                                                                                                                                                                                                                                             (KONN ) GIST-BROCADES NV.
                                                                                                                    elongation factor; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               991 CGG---GACACCCGGAACTGCACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGAT 1047.
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CACATCCTCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAG
                                                                                  631 GACATGGTCGACGACGAGCTGCTCGAGCTCGAGCTCGAGGTCCGCGAGCTGCTC
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              Sequence of SrtufR1 gene encoding elfamycin-resistant elingation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 1194;
                                                                                                                                                                                                                                                                                                                                                Heinstra PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.3%; Score 526.2; DB 13; Length 67.2%; Pred. No. 5.6e-101; tive 0; Mismatches 353; Indels
                                                        Elfamycin resistant actinomycetes; antibiotic resistant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         transform streptomycetes to resistant pheno-type
                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                             Bosch L,
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                                                                                                 Streptomyces ramocissimus
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                          factor EF-TuR Thr 378
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                 571 CACATCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAG 630
                                                                             751 CTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTAC 810
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                                                                                                                                                                                                                                                                                                    751 AAGACCGAGAAGACCACCACCACGGTCACGGCATCGAGATGTTCCGCAAGCTGCTCGAC 810
481 TCCGAGTACGAGTTCCCGGGCGACGACCTGCCGGTCGTCCGCGTCTCCGCGTCTGAAGGCG
                                                                                                       CTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTAC
                                                                                                                                                                                 631 AAGCCGTTCCTCATGCCGATCGAGGACGTCTTCACGATCACCGGTCGCGGCACGGTCGTC
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                                             AGCAACTACGAGTACGACGGCGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGCG
                                                                                                                                     ----GGCGACGCTCAGTGGACGCAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. of elfamycin by actinomycetes is removed by mutating the gene tuf into tuff sencoding a protein esistant to an elfamycin, pref. mociangin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGACCACGGAAAGACCACTCTCACCGCCGCGCTCATGGTGCT-----CGCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 526.2; DB 13; Length 1194;
Pred. No. 5.6e-101;
0; Mismatches 353; Indels 54;
                                                                                                                                                                                                                                                                                       Heinstra PW;
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                                                                                                                                                                                                                                                                                       Kerkman R, Bosch L, Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                                                               transform streptomycetes to resistant pheno-type
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.3%;
Best Local Similarity 67.2%;
Matches 832; Conservative (
                                                                                                                                                                               91EP-0201702
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90EP-0201851
                               Streptomyces ramocissimus.
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 elongation factor; ss
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
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   181 TCCGAGTACGAGTTCCCGGGCGACGACCTGCCGGTCGTCCGCGTCTCCGCGCTGAAGGCG 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CACGTCGACTGCCCGGGTCACGCGGACTACATCAAGAACATGATCACGGGTGCGGCGCAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            631 GACATGGTCGACGAGGAGCTGCTCGAGCTCGTCGAGCTCGAGGTCCGCGAGCTGCTC 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   691 AGCAACTACGAGTACGACGCGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGCG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. Of elfamycin by actinomycetes is removed by mutating the gene tuf into tuff encoding a protein resistant to an elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCGGACCTGAACGAGGCCACCCCGTTCGACAACATCGACAAGGCTCCTGAGGAGCGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571 CACATCCTCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 1194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54;
                                                                                                                                                                                                                                                         PW;
                                                                                                                                                                                                                                                         Heinstra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 31.2%; Score 524.6; DB 13; Length Best Local Similarity 67.1%; Pred. No. 1.2e-100; Matches 831; Conservative 0; Mismatches 354; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1194 BP; 238 A; 404 C; 373 G; 179 T; 0 other;
                                                                                                                                                                                                                                                       Luiten RGM, Kerkman R, Bosch L, Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                               New protein conferring resistance to elfamycin - transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Pages 13-15; 35pp; English.
                                                                                                                           91EP-0201702.
                                                                                                                                                               91EP-0201702.
90EP-0201851.
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                                                                                                                           02-JUL-1991;
                                                                                                                                                             02-JUL-1991;
                                                                                                                                                                                10-JUL-1990;
                                                                                          15-JAN-1992
                                                    EP466251-A
                                                                                                                                                                                                                                                                          Woudt LP;
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the protection and the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6881 AIGGACGCCCATCCTCGTGGTTGCTGCTACCGACGCCCCGATGCCTCAGACTCGCGAG 6940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 GICGACCACGGAAAGACCACICICACCGCCGCGCTCACCAIGGIGCI-----CGCCTCC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 CGCGGTATCACCATCAACACCGCCACCGTCGAGTACGAGACCGAGACCCGCCACTACGCA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 ATGGACGGTGCCATCCTCGTCGTATCCGGTGCCGACGGGCCCATGCCGCAGACCAAAGAG 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 CACGTCGACTCCCCGGCCACGCCGACTATGTCAAGAATATGATCACCGGCGCTGCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAS59506-AAS59804 represent DNA molecules encoding
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31.2%; Score 524; DB 23; Length 29
Best Local Similarity 66.6%; Pred. No. 3.7e-100;
Matches 837; Conservative 0; Mismatches 365; Indels
                                                                                                                                                                                                                                                                         Bhatia A;
                                                                                                                                                                                                                                                                    Wang SS,
                                                                                                                                                                                                                                                                                                                         Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 5; 1069pp; English.
                                                                                                                                                                                                                                                                                   Mitcham JL,
                                                                                                                                                                                                                                                                                                                         Jen S,
21-APR-2000; 2000US-199047P. 02-JUN-2000; 2000US-208841P. 07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                              Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating acne vulgaris -
                                                                                                                                                                                                                                                                                   Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-616774/71.
                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                   L'maisonneuve J,
                                                                                                                                                                                                                                                                                   Skeiky YAW,
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1288 GACAAGGATGAGGAGGCGAAGATGTGCATGCCTGGTGACCGTATCAAAATGATTGTTCAG 1347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1108 GAAAGAGGCATGGTGCTGGCAAAGCCTGGCTCTATCACACCGCACCACCAAGTTTGAGGCT 1167-
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                                                                                                                                                                                                                                                                                                           7211 AAGCCCTTCCTTATGCCGATCGAGGACGTCTTCACCATCACCGGCCGTGGCACCGTTGTC 7270
                                                                                                                                                                                                                                                                                                                                                                              7271 ACCGGTCGTGTGCAGCGCGCGTCGTCAAGACTGGCGAAGAGGTCGAGATCGTCGTATC 7330
                                                                                                                                                                                                                                                                                                                                                                                                                 991 C---GGGACACCCGGAACTGCACGGTCACTGGTGTGAGATGTTCCAGAAGACCATGGAT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                     1048 GATGCCATGGCCGGAGACAATGTTGGGCTGCTGCTCCGTGGTATGCAGAAGGATGACATT 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1168 GTTGTGTATGTGCTTAAGAAGGAAGAGGTGGCCGACACTCACCTTTCTTCCCTGGTTAC 1227
                                                                                         -------GGTGATGAGAAGTGGACCCAGTCG 7150
                                                                                                                                                                                                                                                                          871 CICCCGIICIIGCICGCIGIIGAAGAIGICIICICCCAICACGGICGIGGIACAGIIGCC 930
                                                                                                                                                                                                                                                                                                                                             931 ACTGGCCGTATAGAGCGTGGCACCGTCAAGATTGGTGACACACAGTCGATATCGTCGGAATC 990
                                                                 691 AGCAACTACGAGTACGACGACGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGCG 750
                                                                                                                                                                                                     811 ATCTTCTCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTCCCGCAGAGGCAGACTGAC 870
631 GACATGGTCGACGACGAGGAGCTGCTCGAGCTCGTGGAGCTCGAGGTCCGCGAGCTGCTC 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa DNA for cellular proliferation protein #398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1408 ACCGTTGGTGCCGGTGTCATCAACAAATCATTGAGTAAACTGGATATAACATATC 1463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; ds; prokaryotic cellular proliferation gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS54267 standard; DNA; 1194 BP
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                                                                                                                                                                             7121 CTCCAG------
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                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes thanselves and the discovery of novel antibiotics, the essential genes thanselves and the encoded proteins. The prokaryotes used are netwinding, pseudomonas aeruginosa and Enterococcus faccalis. The promeunoniae, pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets of or antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery for homologous nucleic acids which are required for cell proliferation in essential prokaryotic callular proliferation protein.

Commanded the printed specification, but was obtained in electronic command directly from MIPO at the way obtained in electronic commanded to the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                    Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 GGCGAGGGGCAAGTTCGAGCGCACCAAACCACATCATAAGATAGGCACCATCGT 278
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                                                                                                                                                                                                                                                                                              polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                antibiotics, comprise sequences of antisense nucleic acids
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Pred. No. 5.2e-100;
0; Mismatches 384; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1194 BP; 260 A; 362 C; 350 G; 222 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       Claim 27; Seq ID No 7904; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                             2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                                                                22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
                                                     21-MAR-2001; 2001WO-US09180.
                                                                                   2000US-191078P.
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  WO200170955-A2
                                                                                                                                                                                                                    Haselbeck R,
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                                                                                 21-MAR-2000;
                                                                                                             26-MAY-2000;
                                                                                                                        23-OCT-2000;
                                                                                                                                      27-NOV-2000;
                            27-SEP-2001.
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GGTGCTGGCAAAGCCTGGCTCTATCACACCGCACACAAGTTTGAGGCTGTTGTGTATGT 1178 -
                         1059 CGGAGACAATGTTGGGCTGCTGCTCCGTGGTATGCAGAAGGATGACATTGAAAGAGGCAT 1118
519 TGCCATCCTCGTATCCGGTGCCGACGGCCCCATGCCGCAGACCAAAGAGCACATCCT 578
                                                                                  579 CCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAGGACATGGT 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 GTCGGTGGCAGCGCGCCTAAGAAGTACGACGAGATCGACGCCGCCCCCGAGGAGCGCGCC 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. of elfamycin by actinomycetes is removed by mutating the gene tuf into tuff encoding a protein resistant to an elfamycin, pref. mocimycin (kircomycin). The inventors claim EF-TuR and the genes (tufk) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACGTCGACTGCCCCGGCCACGCCGACTATGTCAAGAATATGATCACCGGCGCTGCGCAG
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of SrtufRl gene encoding elfamycin-resistant elingation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.8%; Score 518.2; DB 13; Length 1194;
llarity 66.7%; Pred. No. 2.7e-99;
Conservative 0; Mismatches 358; Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                        Luiten RGM, Kerkman R, Bosch L, Vijgenboom E, Heinstra
                                               Elfamycin resistant actinomycetes; antibiotic resistant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein conferring resistance to elfamycin - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Pages 13-15; 35pp; English.
                                                                                                                                  Location/Qualifiers 4..1194
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90EP-0201851.
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                                                                                                   Streptomyces ramocissimus
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                                                                                                                                                                   /*tag=
                                                                elongation factor; ss.
               factor EF-TuR Pro 278
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591 AGCAACTACGAGTACGACGACGACGTACCAATCGTCGCTGGCTCGCCCTCAAGGCG 750
                                                                                                                                            CTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTAC 810
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                                                                                                                                                                                                                                                                                                                                              AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli prolliferation. AAA65890 to AAA66055 and AAB15886 to AAB16040 represent nucleotide and protein sequences associated with E. coli prolliferation. AAA66056 and AAA66057 represent primers used for sequencing E. coli prolliferation inhibiting nucleotide inserts in an example from the present invention. Methods from the present invention can be used to identify a prolliferation. required gene in a microorganism, by contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                a microorganism with a proliferation required gene activity inhibitory nucleic acid identified in another organism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can be used for antisense therapy for killing bacteria.
                                                                                                                                                                             Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 GCGCCGAGGCCAAGTTCGAGCGCACCAAACCACATCGACATAGGCACCATCGGCCAT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCGACCACGGAAAGACCACTCTCACCGCCGCGCTCACCATGGTGCTCGCCTCCGTCGGT 336
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                                                                                                                                                                                                                                                            Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCGACGACGAGGAGCTGCTCGAGCTCGAGCTCGAGGTCCGCGAGCTGCTCAGCAAC 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.3%; Score 508.8; DB 21; Length 1185;
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                                                                                                                                                                        Trawick J, Forsyth RA, Froelich JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 382; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1185 BP; 286 A; 306 C; 325 G; 268 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.5e-97;
                                                                                                                                                                                                                                                                                                                    Claim 8; Page 115; 316pp; English.
                                                                                     27-JAN-2000; 2000WO-US02200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%;
                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  803; Conservative
                                                                                                                                                                       Ohlsen KL,
                                                                                                                                                                                       Xu HH;
                                                                                                                                                                                                                 2000-514822/46.
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 Escherichia coli.
                                                                                                                                                                                                                                  P-PSDB; AAB15890
                            WO200044906-A2
                                                                                                                                                                       Zyskind J, O
Yamamoto RT,
                                                                                                                27-JAN-1999;
                                                         03-AUG-2000
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1177 GIGCTTAAGAAGGAAGAGGGIGGCCGACACTCACCTTTCTTCCTGGTTACCGCCCACAG 1236
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                                  421 GTTGATGACGAGGAGCTGCTGGAACTGGTTGAAATGGAAGTTCGTGAACTTCTGTCTCAG 480
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                                                                                                                                                                               481 TACGACTICCCGGGCGACGACACICCGAICGITCGIGGITCTGCICTGAAAGCGCIGGA-
                                                                                                                                                                                                                                                                                                                                                                                                     817 TCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTCCCGCAGAGGCAGACTGACCTCCCG
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                                                                                                                                                                                                                                                    757 GCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTACATCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1057 GCCGGAGACAATGTTGGGCTGCTGCTCGTGTATGCAGAAGGATGACATTGAAAGAGGC
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Escherichia coli nucleotide sequence SEQ ID NO:698.
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GCCGGTGTCATCAACAAATCATTGAGTAA 1446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for generating a reperiory or nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microrganisms e.g. algae, archaea, bacteria, fungil and parasitical species, ganus, family and group. A nucleic acid (1) and parasitical species, ganus, family and group. A nucleic acid (1) and parasitical species, ganus, family and group. A nucleic acid (1) and parasitical species, ganus, family and group. A nucleic acid (1) and parasitical species, ganus, family and group. A nucleic acid (1) detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at at least one toxin gene. hexA nucleic acids are used for the specific and ubquitous detection and for identification of Streptococcus pneumoniae. (1) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacteriaceae family, Pseudomonads group, Streptococcus sp., Corynebacteriaceae family, Pseudomonads group, Streptococcus sp., Naisseria gonornhoeae and Stabhjoroccus sp., Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes a method for generating a repertory of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 GACTGCCCCGGCCACGCCGACTATGTCAAGAATATGATCACCGGCGCGTGCGCAGATGGAC 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid sequences are used to generate universal probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 508.8; DB 22; Length 1185;
Pred, No. 2.5e-97;
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                                                                                                                                                                                                                                                                                                                      Menard C,
                                                                                                                                                                                                                                                                                                                         Boissinot M, Huletsky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 803; 1580pp; English.
                                                                                                                                                                                                                                                                            (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
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65.3%;
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            Escherichia coli.
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                                                                                                                           GITGAIGACGAAGAGCIGCIGGAACIGGITGAAAIGGAAGIICGIGAACIICIGICICAG 480
                          517 GGTGCCATCCTCGTCGTATCCGGTGCCGACGGGCCCATGCCGCAGACCAAAGAGCACATC
                                                                                                                                                                                                 GTCGACGACGAGCTGCTCGAGCTCGTCGAGCTCGAGGTCCGCGAGCTGCTCAGCAAC
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                                                                                                CTCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAGGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the ancoded proteins. The prokaryotes used are Escherichia coli, Staphylococus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonnas aeruginosa and Enterococus faccalis. The proteinoniae, Pseudomonnas aeruginosa and Enterococus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to intended to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Sesential prokaryotic cellular proliferation protein.

Oute: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic for the control of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 GICGACCACGGAAAGACCACICICACCGCGCGCGTCACCAIGGIGCICGCCICCGTCGGI 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 508.8; DB 23; Length 1185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                              Trawick JD,
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0; Mismatches 382; Indels
                                                                           Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                                           E. coli DNA for cellular proliferation protein #350.
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Matches 803; Conservative
                 (first entry)
                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
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                                                                                                                     Escherichia coli.
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22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto RT,
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997 ACCCGGAACTGCACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGATGATGCCATG 1056
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are bechariotic speudonas aeruqinosa and Enterococcus facellis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to adentify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23; Length 1230;
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                                                                                                                                     Salmonella typhi DNA for cellular proliferation protein #262.
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                                                                                                                                                                      Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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Pred. No. 1.2e-96;
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Xu HH;
                                  AAS56229 standard; DNA; 1230 BP
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2000US-206848P.
2000US-207727P.
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2001US-269308P.
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26-MAY-2000;
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RESULT 15
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Secale cereale
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Secale
; Triticeae; Secale
; Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Hattori
J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 12-SEP-2000
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//dev_Stage="seedling three-leaf stage"
//note="vector: Bluescript SK-/xhoI-EcoRI; Site_1: Eco RI;
Site_2: Xho I; Sampled three-leaf seedlings treated for
one week at 20C, 12 hrs light/day. Library made with
Stratagene UNLSAP XR kit/Gigapack III Gold Kit. Lambda
library is amplified, then mass excised in SOLR cells. "
243 c 187 g 190 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
                                                                                                                                1451 GATATAACATATCCACCATGAGAATTTTCCTTGTTTACTCAAAGCGACATGCTCCGTAGT 1510
                                                                                                                                                            1391 TCCGTGAGGGTGGTAAGACCGTTGGTGCCGGTGTCATCAACAAATCATTGAGTAAACTG 1450
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                                                                                                                                                                                                                                                                                                               1571 ITTGTCAAGTGAATTTGCATAATTTATGACATTCACGACAAAGATTCACATATCTGGTTG 1630
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SC01_03a09_A SC01_AAFC_ECORC_cold_stressed_winter_rye_seedlings
Scoil_cereale cDNA clone Sc01_03a09, mRNA sequence.
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                                                                 841 TCAAGAIGGITGITCAGCICAICCAGCCTGITGCITGIGAGCAGGGIATGAGGITTGCTA 900
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/clone="Sc01_03a09"
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Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
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AI665388 624 bp mRNA linear EST 02-FEB-2000 605010F02.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
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                                 809 ACATCTTCTCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTCCCGCAGAGGCAGACTG
                                                     CCACTGGCCGTATAGAGCGTGGCACCGTCAAGATTGGTGACACAGTCGATATCGTCGGAA
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A1665388
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/db_xref="taxon-1577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/tissue_type="nucellar, embryo, and endosperm"
/tassue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
/tite_2: XhoI; Kernel endosperm cDNA library from Schmidt
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Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Fax: 650 725 8221
Fax: 605010 row: F column: 02.
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94.8%;
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/tissuc_type="developing seeds"
/dev.stage="15 days after anthesis"
/lab_host="E. coll DH10B"
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: Not1; Site_2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"
                                     BQ245968 681 bp mRNA linear EST 03-MAY-2002 TaE15017G12R TaE15 Triticum aestivum cDNA clone TaE15017G12R, mRNA
                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
1 (bases 1 to 681)
                                                                                                                                                                                                                                                                                                            Wheat functional genomics - Glenlea developing seeds cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGATGATGCCATTGCTGGGGACAA 300
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Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
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86.9%; Pred. No. 3.8
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/db_xref="taxon:4565"
/clone="TaE15017G12R"
/clone_lib="TaE15"
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Eukaryota; Viridiplanta; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplanta; Streptophyta; Enliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.

7 Triticeae; Hordeum.

1 (bases 1 to 736)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin:
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 18-JAN-2002
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/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/ 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV943931 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah19917 3', mRNA sequence.
                                                                                                                                         GGAAGAGGGTGGCCGACACTCACCTTTCTTCCCTGGTTACCGCCCACAGTTCTACATGCG 1247
                                                                                                                                                                                                                        1308 GATGTGCAFGCCTGGTGACCGTATCAAAATGATTGTTCAGCTCATCCAGCCTGTTGCTTG 1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.1%; Score 523.4; DB 1/86.1%; Pred. No. 2.5e-94; iive 0; Mismatches 91
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Hordeum vulgare subsp. spontaneum
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/db_xref="taxon:77009"
/clone="bah19917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tshini@genes.nig.ac.jp.
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EST 09-APR-2002
/clone="Sc01_11c12"
/clone_lib="Sc01_AAFC_ECORC_cold_stressed_winter_rye_seed1
                                                                    /dev_stage="seedling three-leaf stage"
/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;
Site_2: Xho I; Sampled three-leaf seedlings treated for
one week at 20C, 12 hrs light/day. Library made with
Stratagene UNIZAP XR kit/Gigppack III Gold kit. Lambda
library is amplified, then mass excised in SOLR cells. "
227 c 178 g 127 t 35 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1454 ATAACATATCCACCATGAGAATTTTCCTTGTTTACTC-AAAGCGACATGCTCCGTAGTTG 1512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 CAACCATINIGANCGNCAAGGATGAGGAGGCGAAGATGTGCATGCCGGGTGCCCGTATCA 220
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                                                                                                                                                                                                                                                                                                                                                                                                                             854 CGCAGAGGCAGACTGACCTCCCGTTCTTGCTCGCTGTTGAAGATGTCTTCTCCATCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCGTGGTACAGTTGCCACTGGCCGTATAGAGCGTGGCACCGTCAAGATTGGTGACACAG
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                                                                                                                                                                                                                                                                                                                                              794 ATGAGTGGGTCGACTACATCTTCTCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTCC
                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                               Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                   31.0%; Score 521.2; DB 12; Length
80.1%; Pred. No. 6.8e-94;
.ive 5; Mismatches 140; Indels
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                                                         /tissue_type="leaf, crown"
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; Triticeae; Secale.
[ (bases 1 to 761)
Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouelle,T., Robert,L.S., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear EST 12-SEP-2000
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KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sc01_11c12_A Sc01_AAFC_ECORC_cold_stressed_winter_rye_seedlings
Secale cereale cDNA clone Sc01_11c12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                           1263 AGGGAGTGTGACTACGATTATGAATGACAAGGATGAGGAGGGGGAAGATGTGCATGCCTGG 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                        1323 TGACCGTATCAAAATGATTGTTCAGCTCATCCAGCCTGTTGCTTGTGAGCAGGGTATGAG 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1383 GITTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGCCGGTGTCATCAACAAATCATTGA 1442
                                                                                                                                                                                                                                                                         1203 ACACTCACCTTTCTTCCCTGGTTACCGCCCACAGTTCTACATGCGGACAACTGATGTGAC 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1443 GTAAACTGGATATAACATATCCACCATGAGAATTTTCCTTGTTTACTC-AAAGCGACATG 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1502 CTCCGTAGTTGTTATGTGGTGAGTTTTAGGGGTTGCTCATGTGCAATTGTAGTATGA 1561
                                                                                                           CCGTGGTATGCAGAAGGATGACATTGAAAGAGGCATGGTGCTGGCAAAGCCTGGCTCTAT 1142
                                                                                                                                                                                          1023 TGAGATGTTCCAGAAGACCATGGATGATGCCATGGCCGGAGACAATGTTGGGCTGCTGCT 1082
                                                                                                                                                                                                                                                                                               376 GGGGAACGTGACAAACATTATGAATGACAAGGATGAGGAGGCCAAGATGTGCATGCCGGG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 GTAAAGTGGATGGAGGATATCCACGTGAGAATTTTCCTCATTTACTCTTTGCGAAATG 137
                                                                                                                                496 CACGCCACACACCAAGTTTGAGGCAGTTGTGTATGTGCTCAAGAAGGAGGAGGGTGGCCG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .136 CTATGTAGTTGTTATTATGCG-----TTTAGGGAAGGCTCTTGTGAAATTGTAGTATGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1562 CACTITITITITIGCAAGIGAATITIGCATAATITATGACATTCACGACAAAGATTCA 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 CACATITITCT -- TCAAGTGAAATTGCATACTTTGTAGTATTCACGACAAAGGTACA 28
                                                   Eastern Cereal and Oilseed Research Centre
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/db_xref="taxon:4550"
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BE705674.1 GI:10093939
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Fax: (613) 759-1701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secale cereale
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460

Gaps

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/clone_lib="Y. Ogihara unpublished cDNA library, Wh_yd"
/tissue_type="spikelet at late flowering"
/dev_stage="Feekes' scale 6"
/dev_stage="Feekes' scale 6"
/note="Wector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: Ecoth: Site_2: Xho1; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab): Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1059 CGGAGACAATGTTGGGCTGCTGCTCCGTGGTATGCAGAAGGATGACATTGAAAGAGGCAT 1118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 939 TATAGAGCGTGGCACCGTCAAGATTGGTGACACAGTCGATATCGTCGGAAATCCGGGACAC 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ308303 Y. Ogihara unpublished cDNA library, Wh_yd Triticum aestivum cDNA clone whyd15914 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.9%; Score 520; DB 13; Length 728; 86.3%; Pred. No. 1.2e-93;
                                                                                                                                                                                                                                                                                                                              Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whyd15g14"
                                                                                                                                                                                                                                                             Expressed genes in Triticum aestivum Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                BJ308303.1 GI:20116830
                                                                                                                                                                                                                                           Ogihara, Y. and Murai, K.
                                                                                                                                                                                                    Triticeae; Triticum. (bases 1 to 728)
                                                                                                                                                                                                                                                                                                            Contact: Tadasu Shin-i
                                                                                                                                   Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635; Conservative
                                                                                                            bread wheat.
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Hordeum vulgare
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu, Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear EST 22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot CDNA
GGAGGCGAAGATGTGCATGCCTGGTGACCGTATCAAAATGATTGTTCAGCTCATCCAGCC 1358
                                                                                                                                                             1359 TGTTGCTTGTGAGCAGGGTATGAGGTTTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGC 1418
                                                                                                                                                                                                                                            1419 CGGTGTCATCAACAAAATCATTGAGTAAACTGGATATAACATATCCACCATGAGAATTTT 1478
                                                                                                                                                                                                                                                                                                                           1479 CCTIGITIACIC-AAAGCGACAIGCICCGIAGIIGIIAITAIGIGGIGAGIITIAGGGGI 1537
                                                                                                                                                                                                                                                                                                                                                                                                          1538 TGCTCATGTGCAATTGTAGTATGACACTTTTTTTTTTGTCAAGTGAATTTGCATAATTTAT 1597
                                                                                                      /clone_lib="Hordeum vulgare seedling shoot EST library HvcNNA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
                                                                                                                                                                                           248 CGTGGCTTGTGGGGGAATGAGGTTTGCCATCCGTGAAGGTGGCAAGACCGTCGGTGC 189
                                                                                                                                                                                                                                                                                  188 CGGTGTCATCAATAATCATTCAGTAAAGTGGATGGAGGATATCCACCGTGAGAATTTT 129
                                                                                                                                                                                                                                                                                                                                                    HVSMEb0020G16f Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMEb0020G16f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dq 006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: AATTAACCCTCACTAAAGGG
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/clone="HVSMEb0020G16f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ity sequence stop: 739.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start:
High quality sequence stop: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG301275
BG301275.1 GI:13098802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1598 GACATTCACGACAAAG 1613
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 AGTATTCACGACAAAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare.
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/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, YU, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or breath and sequence has been trimmed to sequence and contains and sequence has been trimmed to sequence and contains and sequence has been trimmed to sequence and contains a minimum of 100 bases of phred value 20 or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 258 c 212 g 205 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               794 ATGAGTGGGTCGACTACATCTTCTCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence analysis see
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/clone="whh13j1".
/clone="whh13j1".
/clone=lib="Y. Ogihara unpublished cDNA library, Wh_h"
/tissue_type="spike at heading date"
/tesue_type="spike at heading date"
/dev_stage="reekes' scale 10.5"
/note="vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoroR; Site_2: Xho!; Plants were grown under
Nydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 08-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä,
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                                                                                                     1393 CGTGAGGGTGGTAAGACCGTTGGTGCCGGTGTCATCAACAAAATCATTGAGTAAACTGGA 1452
                                                                                                                                                                                                                                                                                                       GTTATTATGTGGGTGAGTTTTAGGGGTTGCTCATGTGCAATTGTAGTATGACACTTTTTT 1571
1333 AAAATGATTGTTCAGCTCATCCAGCCTGTTGCTTGTGAGCAGGGTATGAGGTTTGCTATC 1392
                                                                                                                                                                                                    1453 TATAACATATCCACCATGAGAATTTTCCTTGTTTACTC-AAAGCGACATGCTCCGTAGTT 1511
                                                                                                                                                    219 CGTGAAGACGGCAAGACAGTCGGTGCAGGTGTCATCAACACATTTCAGTAAAGTGGA 160
                                                                                                                                                                                                                               AAGATGGTTGTGGAGCTCATCCAGCCTGTGGCTTGTGAGCAGGGAATTAGGTTTGCCATC 220
                                                                                                                                                                                                                                                                                                                                                         99 GCTATTATG-----GGTTTAGGGAAGGCTCTTGTGAAATTGTAGTATGGCTCATTCTTC -46
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BJ263237.1 GI:20084049
EST.
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                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                            1572 TTGTCAAGTGAATTTGCATAATTTATGACATTCACGACAAAGA 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum aestivum"
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/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Ogihara, Y. and Murai, K
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Best Local Similarity 86.4%;
Matches 598; Conservative
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BJ263237/c
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TITLE
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COMMENT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaea; Triticum.

1 (basea 1 to 658)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
(Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BJ302467 BJ302467 Y. Ogihara unpublished cDNA library, Wh_yd Triticum aestivum cDNA clone whydl5g14 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             959 AGATTGGTGACACAGTCGATATCGTCGGAATCCGGGACACCCGGAACTGCACGGTCACTG 1018
                                                                                                                                            1019 GTGTTGAGATGTTCCAGAAGACCATGGATGATGCCATGGCCGGAGACAATGTTGGGCTGC 1078
                                                                                                                                                                                                                 1079 IGCICCGIGGIAIGCAGAAGGAIGACAITGAAAGAGGCAIGGIGCIGGCAAAGCCIGGCT 1138
                                                                                                                                                                                                                                                                                     1199 GCCGACACTCCACCTTTCTTCCCTGGTTACCGCCCACAGTTCTACATGCGGACAACTGATG 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1319 CTGGTGACCGTATCAAAATGATTGTTCAGCTCATCCAGCCTGTTGCTTGTGAGCAGGGTA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1379 TGAGGTTTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGCCGGTGTCATCAACAAATCA 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1439 TTGAGTAAACTGGATATAACATATCCACCATGAGAATTTTCCTTGTTTACTC-AAAGCGA 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1498 CATGCTCCGTAGTTGTTATTATGTGGTGAGTTTTAGGGGTTGCTCATGTGCAATTGTAGT 1557
                                                                                          899 TCTTCTCCATCACCGGTCGTACAGTTGCCACTGGCCGTATAGAGCGTGGCACGTCA 958
                                                                                                                                                                                                                                                                                                                                                                                205 TGAGGTTTGCCATCCGTGAAGGTGGCAAGACCGTCGGTGCCGGTGTCATCATATATCA 146
                                   685 TCTTCTCCATCACTGGTCGTGGTACAGTTGCCACTGGCCGTATCGAGCGTGGCACCGTCA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 CGGGTGACCGTATCAAGATGGTTGTGGAGCTCATCCAGCCCGTGGCTTGTGAGCAGGGAA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 TTCAGTAAAGTGGATGGAGGATATCCACCGTGAGAATTTTCCTCATTTACTCTTTTGCGA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Far: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1558 ATGACACTTTTTTTTTTGTCAAGTGAATTTGCA 1589
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BJ302467
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TITLE
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/clone_lbp="". Ogihara unpublished cDNA library, Wh_yd"
/tissue_type="spikelet at late flowering"
/dev_stage="Feekes' scale 6"
/dev_stage="Feekes' scale 6"
/note="Vector: Lambda Uni ZAP XR, excised phagemid;
Site_1: EcoRI: Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ close lab
at the University of California, Riverside (Akhunov, Chin
/ Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.2%; Score 507.4; DB 13; Length 658; Best Local Similarity 86.8%; Pred. No. 4e-91; Matches 570; Conservative 0; Mismatches 86; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               731 CTGGCTCCGCCCTCAAGGCGCTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGGG 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        791 ACGAIGAGIGGGICGACIACAICTICICGITGGITGAIAAAGIGGAITCCIAIAIICCAG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    851 TCCCGCAGAGGCAGACTGACCTCCCGTTCTTGCTCGCTGTTGAAGATGTCTTCTCCATCA 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 CCGGTCGTGGTACAGTTGCCACTGGCCGTATAGAGCGTGGCACCGTCAAGATTGGTGACA 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1331 TCAAAATGATTGTTCAGCTCATCCAGCCTGTTGTGAGCAGGGTATGAGGTTTG 1387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 CAGTCGACCTCGTCGGCATCAGGGAGACTCGCAATGCCACGGTCACTGGTTGAGATGT
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                                                                              /organism="Triticum aestivum"
                                                                                                        /cultivar="Chinese Spring"/db_xref="taxon:4565"
Email: tshini@genes.nig.ac.jp.
                             Location/Qualifiers
                                                                                                                                                                      /clone="whyd15g14"
                                                          source
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us-09-810-764a-6.rst

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426

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GACGCCCCCCGAGGAGCGCCCGCGCGGTATCACCATCAACACCGCCACCGTCGAGTAC

427 GAGACCGAGACCCGCCACTACGCACACGTCGACTGCCCCGGCCACGCCGACTATGTCAAG

61 GCGCTCACCATGGTGCTCCCTCCGTCGGGGGCAGCGCCCCAAGAAGTACGACGAGTC

307 GCGCTCACCATGGTGCTCGCCTCCGTCGGTGGCAGCGCCCTAAGAAGTACGACGAGATC

δ

240

486

300

AATATGATCACCGGCGCTGCGCAGATGGACGGTGCCATCCTCGTCGTATCCGGGTGCCGAC

487

g ò g δ g ò

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547

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GAGCTCGAGGTCCGCGAGCTGCTCAGCAACTACGAGTACGACGGCGACGACGTACCAATC 726

299

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607 ATCGTTGTCTTCCTCAACAAGAAGGACATGGTCGACGAGGAGGAGCTGCTCGAGCTCGTC

481 GTCTCCGGCTCTGCACTCAGAGCGCTCGAGGCCCTCATGGCCACCCCTGGCCTCAAGCGT 540

GTCGCTGGCTCCGCCCTCAAGGCGCTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGC

727

g

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847 CCAGTCCCGCAGAGGCAGACTGACCT - CCCGTTCTTGCTCGCTGTTGAAGATGT - CTTCT

846

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/lab.host—"TJC121"
//note—"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Xhoi; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, YU, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and eabove. For more details on library preparation and
                                                                                                                                                                                                                                                   Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

Triticeae; Hordeum.

Triticeae; Hordeum.

Wing, R., Close, T.J.,
Wing, R., Close, T.J.,
Wing, R., Close, T.J.,
J., Oates, R. and Main, D.
J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library
Unpublished (2001)
                                                         EST 22-0CT-2001
                                                                     HVSNEn0020M20f Hordeum vulgare rachis EST library HVCDNA0015 (normal) Hordeum vulgare CDNA clone HVSMEn0020M20f, mRNA sequence. B1959687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
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                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 556.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4513"
/clone="HVSMEn0020M20f"
                                                      678 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Rachis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rwing@clemson.edu
                                                                                                                                                                        BI959687.1 GI:16310942
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86.1%;
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BI959687
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AV938814 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum AV938814
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
1118 11-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                       Hordeum vulgare subsp. spontaneum Hordeum vulgare subsp. spontaneum
                                                                                                                                                                                                                                                                   AV938814.1 GI:18234611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                Triticeae; Hordeum. (bases 1 to 644)
                                                    905 CCATCACCGGT 915
                                                                                      661 CCATCAACGGT 671
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JOURNAL
COMMENT
                601
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AV938814
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Matches 578; Conservative

Best Local Similarity

Query Match

5

5;

Score 501.4; DB 13; Length Pred. No. 6.2e-90; 0; Mismatches 91; Indels

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250 GACCGTATCAAGATGGTTGTGGGAGCTCATCCAGCCCGTGGCTTGTGAGCAGGGAATGAGG 191
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/db_xref="taxon:4565"
/clone="whf23e11"
                                                                                                                                                                          Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                          source
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                              REFERENCE
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                                                                    /clone="bah19g17"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev.stage="adult, heading stage"
180 c 192 g 141 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1086 TGGTATGCAGAAGGATGACATTGAAAGAGGCATGGTGCTGGCAAAGCCTGGCTCTATCAC 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ255324 BJ255324 Y. Ogihara unpublished cDNA library, Wh_f Triticum aestivum cDNA clone whf23ell 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                          Length 644;
                             /organism="Hordeum vulgare subsp. spontaneum"
                                                                                                                                                                                      Score 500.6; DB 10; Length
Pred. No. 9.1e-90;
0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1146 ACCGCACACCAAGTTTGAGGCTGTTGTGTATGTGCTTAAGAAG 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="H602"
/db_xref="taxon:77009"
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library was made, and the CDNA clones were in vivo excised to give pBluescript phagamids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Y. Ogihara unpublished cDNA library, Wh_f"
/tissue_type="spike at flowering date"
/tissue_type="spike at flowering date"
/dev_stage="feekes' scale 10.5.1"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: Xhoi; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhnov
in J Dvorak Lab): Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
17E1: 81-559-81-6856
Fax: 81-559-81-6855
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Unpublished (1999)
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Wheat functional genomics - Thatcher LrI cDNA library
Unpublished (2001)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average inset size is >2.2 kb
Plate: 167 row: E column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Leaf tissue"
/dev stage="14 Days old"
/lab_host="E. coll XLOLK"
/note="Vector: Lambda ZapII; mass excised in plasmid
vector pBK-CMV (Stratagene).; Site_1: EcoRI, Site_2: XhoI:
mRNA obtained from wheat NIL Thatcher Lrl 24 hours after
innoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avizulence gene Avrl."
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1384 TTTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGCCGGTGTCATCAACAAAATCATTGAG 1443
                                                                                                                                      1503 TCCGTAGTIGTTATTATGTGGTGAGTTTTTAGGGGTTGCTCATGTGCAATTGTAGTATGAC 1562
                         190 TITGCCATCCGTGAAGGTGGCAAGACCGTCGTGCTGCTCATCAATAATATCAG 131
                                                                                       BG908358 632 bp mRNA linear EST 05-JUN
TaLr1167E03R TaLr1 Triticum aestivum cDNA clone TaLr1167E03 5'
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                                                                   1444 TAAACTGGATATAACATATCCACCATGAGAATTTTCCTTGTTTACTC-AAAGCGACATGC
                                                                                                                                                            Score 497.6; DB 12; Length 632;
Pred. No. 3.6e-89;
0; Mismatches 79; Indels 0;
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/cultivar="Thatcher Lr1"
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/clone="TaLr1167E03"
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Seg primer: M13 Reverse.
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Best Local Similarity 87.3%;
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                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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102065H09.x1 1020 - Unigene II from Maize Genome Project Zea mays BI992656
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/db_xref="taxon:4577"
/clone_lib="1020 - unique II from Maize Genome Project"
/note="This library represents the unique genes found in
the second round of EST sequencing at Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 CGCCCGCGGTATCACCATCAACACCGCCACCGTCGAGTACGAGACCGGAGACCCGCCACTA 446
                                                                                                                                                              687 GCTCAGCAACTACGAGGTACGACGCGACGTACCAATCGTCGCTGGCTCCGCCCTCAA 746
249 CCAGATGGACGGCGCCATCCTCGTCGTCGTCGCGCCCGACGACCCCATGCCGCAGACCAA 308
                                                                                                                                                                                                                                                                                                                      548
                                                                                                                                                                                                                                                                                                 567 AGAGCACATCCTCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAA 626
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                                                                                                                                     447 CGCACACGTCGACTGCCCCGGCCACGCCGACTATGTCAAGAATATGATCACCGGCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        807 CTACATCTTCTCGTTGGTTGATAAGTGGATTCCTATATTCCAGTCCCGCAGAGGCAGAC
                                                                                                                                                                                                                    507 GCAGATGGACGGTGCCATCCTCGTCGTATCCGGTGCCGACGGGCCCATGCCGCAGACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanford University
855 California Ave, Palo Alto, CA 94304, USA
7721: 650 723 2221
Email: walbortestanford.edu
Plate: 1020065 row: H column: 09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       867 TGACCTCCCGTTCTTGCTCGCTGT 890
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Walbot, V.
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1;
for the maize genome project. Sequences are present from libraries 947 and 949. Contigs were assembled using ZmDBAssembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also selected."
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                                                                                                                                                                                                                                                                              1108 GAAAGAGGCATGGTGCTGGCAAAGCCTGGCTCTATCACACCGCACACCAAGTTTGAGGCT 1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 CTCATCCAGCCTGTTGTTGTGAGCAGGGTATGAGGTTTGCTATCCGTGAGGGTGGTAAG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                          DB 13; Length 558;
                                                                                                                                                                          33; Indels
                                                                                                                                        Score 493.2; DB 1
Pred. No. 2.8e-88;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1588 CATAATTTATGACATTCACG 1607
                                                                                                                                        29.3%;
93.8%;
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                                                                                                                                           Query Match 29.36
Best Local Similarity 93.86
Matches 525; Conservative
                                                                                         BASE COUNT
ORIGIN
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ò g δ Search completed: May 1, 2003, 10:18:51 Job time : 2907 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

1, 2003, 07:08:30 ; Search time 98 Seconds May Run on:

(without alignments) 5260.445 Million cell updates/sec

US-09-810-764A-6

1 atteccaaataateeecaee......gttaaaaaaaaaaaaaaaa 1681 Perfect score: Sequence:

IDENTITY_NUC Scoring table:

Gapop 10.0 , Gapext 1.0

441362 seqs, 153338381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

Issued_Patents_NA: *

/cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			æ			SUMMARIES	
Result No.	ult No.	Score	Query	Length DB	8	ID	Description
	1	488.4	29.1	4	4	US-09-103-840A-1	Sequence 1, Appli
	7	477.4	28.4	44	4	US-09-103-840A-2	Sequence 2, Appli
	m	420.4	25.0	1185	~	US-08-743-637B-185	Seguence 185. App
	4	402.8	24.0		4	US-09-134-001C-2540	Sequence 2540. Ap
	Ŋ	393.2	23.4		4	US-09-218-197-1	Sequence 1, Appli
	9	368.8	21.9		4	US-08-961-527-260	
	7	243.8	14.5		4	US-09-221-017B-642	Sequence 642, App
	œ	188.8	11.2	1230	4	US-09-140-466-1	
ပ	σ	182.2	10.8		7	US-08-920-812-10	10
O	10	182.2	10.8		7	US-08-920-827-10	10,
υ	11	182.2	10.8		Н	US-08-921-177-10	10,
υ	12	182.2	10.8	3719	-	US-08-362-577C-10	10,
O	13	182.2	10.8	m	7	US-08-920-828-10	10,
	14	180.2	10.7		4	US-08-936-165A-87	87,
υ	15	112.6	6.7		4	US-09-556-877-70	70,
υ	16	112.6	6.7		4	US-09-620-412C-70	70,
ပ	17	105.8	6.3	785	٣	US-09-154-083-29	29,
	18	77.8	4.6	390	4	US-09-197-649-7	7, 4
	13	71.4	4.2		_	US-08-125-468-1	H
	50	71.4	4.2	m	7	US-08-474-933-1	7
	21	70.2	4.2	2095	-	US-08-329-681A-2	7
	22	63	3.7	1248	4	US-09-105-537-7	7,
U	23	63	3.7	13613	4	US-09-105-537-3	'n
	24	62.6	3.7	546	4	US-09-194-905-3	m
Ö	25	62.2	3.7	5970	٣	US-09-320-878-21	Sequence 21, Appl
	56	62.2	3.7	6854	4	-194-	7
	27	61.6	3.7	3461	7	US-08-389-564B-1	1,

Sequence 1, Appli	Sequence 3, Appli	Sequence 7, Appl1	1,	Sequence 1, Appli	Sequence 2, Appli	. ,	2,	14,	14,	Sequence 14, Appl	14,	13,	13,	Sequence 13, Appl	Sequence 13, Appl	Sequence 7, Appli	Sequence 7, Appli
US-08-466-047B-1	US-09-174-768-3	US-09-197-649-7	US-08-387-942C-1	US-07-945-283-1	US-09-103-840A-2	US-09-103-840A-1	US-09-311-626B-15	US-08-083-948-14	US-08-393-785-14	US-08-475-694-14	US-08-712-057-14	US-08-083-948-13	US-08-393-785-13	US-08-475-694-13	US-08-712-057-13	US-08-083-948-7	US-08-393-785-7
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3.7	3.7	3.6	3.5	3.5	3.5	3.5	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4
61.6	61.4	9.09	58.6	58.4	58	28	57.6	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4	57.4
28	59	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 785119 ATGGACGGTGCGATCCTGGTGGCCGCCGACGCCCGATGCCCCGAGGCCGCGAG 785178
                                                                               APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRESER, Claire M.
APPLICANT: Traces of the M.
APPLICANT: Trace of INVENTION: TUBERCULOSIS
FILLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 1
LENGTH 4411529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 488.4; DB 4;
Pred. No. 1.5e-103;
0; Mismatches 366;
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium tuberculosis
COTHER INFORMATION: H37Rv
US-09-103-840A-1
                Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%;
65.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 815; Conserva
                                                                   GENERAL INFORMATION:
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Db 785911 TTGATCCAGCCCGTCGCCATGGACGACGATCTGCGTTTCGCGATCCGCGAGGGTGGCCGC 785970
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                                                                                                          -----GGTGACGCGAAGTGGGTTGCCTCT 785385
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571 CACATCCTCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAG 630
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ACTGCCGGAGGGCACCGAGATGGTGATGCCCGGTGACAACACCAACATCTCGGTGAAG
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                                                                                                                                                                                                                                                           CTCGAGGCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTAC
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                                                                                   631 GACATGGTCGACGACGAGGAGCTGCTCGAGCTCGTCGAGCTCGAGGTCCGCGAGCTGCTC
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Fatent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR TITLE OF INVENTION: TUBERCULOSIS
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     787347 IGICGAGGAACIGAIGAACGCGGICGACGAGICGAIICCGGACCCGGICCGCGAGACCGA 787406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 786780 GTGGCGAAGGCGAAGTTCCAGGGACCAAGCCCCACGTCAACATCGGGACCATCGGTCAC 786839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD 786900 CCCGATCTGAACGAGGACGAACGCATTCGACCAGACAACGCCCCCGAGGAGCGTCAG 786959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 GATGGACGGTGCCATCCTCGTCGTATCCGGTGCCGACGGGCCCATGCCGCAGACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630 GGACATGGTCGACGACGAGGAGCTGCTCGAGCTCGAGCTCGAGGTCCGCGAGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              690 CAGCAACTACGAGTACGACGACGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGC
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                                                                                                                                                                                                                                                                                                                                               Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                            Score 477.4; DB 4;
Pred. No. 5.5e-101;
0; Mismatches 366;
                 US/09/103,840A
              CURRENT APPLICATION NUMBER: US/09/103,84
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PAtentIN Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                               28.4%;
ilarity 65.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                       ; OTHER INFORM
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                Matches 815;
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GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
Db 787527 ICGCCCATCGACCACCACCACCGTCACCGGTGTGGAGATGTTCCGCAAGCTGCTCGA 787586
                                                                         Db 787647 CGAGCGTGGCCAGGTTGTCACCAAGCCGGGCACCACGCGGCGCACACACGAGTTCGAAGG 787706
                                                                                                                                                                                                                                                                                 787815 ---ACTGCCGGAGGCACCGAGATGGTGATGCCCGGTGACACACCAACATCTCGGTGAA 787871
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                                                  1047 TGATGCCATGGCCGGAGACAATGTTGGGCTGCTGCTCCGTGGTATGCAGAAGGATGACAT 1106
                                                                                                                                                   1107 TGAAAGAGGCATGGTGGCAAAGCCTGGCTCTATCACACCGCACACCAAGTTTGAGGC 1166
                                                                                                                                                                                                                                                                                                                                                      1227 CCGCCCACAGTTCTACATGCGGACAACTGATGTGACAGGGAGTGTGACTACGATTATGAA 1286
                                                                                                                                                                                                                                                       1167 IGTIGIGIAIGICTTAAGAAGGAAGGGGGGGGCGGACACTCACCTTTCTTCCCTGGTTA 1226
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SOFTWARR: PATENTIN RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
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REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-NOV-1996
FILING DATE: 04-NOV-1996
FIRSTFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 EAST WISCONSIN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 185, Application US/08743637B
Patent No. 5994066
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ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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TELEFAX: (414)277-5591
INFORMATION FOR SEQ ID NO: 185:
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183 TACCATCAACACTTCACACGTTGAATACGATACACCGACTCGCCACTATGCACACGTAGA 242
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                                                                                                                                                                                                                                                                             123 TGGTGCAGCGCGTGCATTCGACCAAATTGATAACGCGCCAGAAGAAAAAGCGCGTGGTAT
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                                                                                                                                                                                                                    45;
                                                                                                                                                                          25.0%; Score 420.4; DB 2; Length 1185; 60.8%; Pred. No. 5.1e-89; tive 0; Mismatches 436; Indels 45;
                                                                                                                   Haemophilus influenzae
                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
LENGTH: 1185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                            al Similarity 60.8 747; Conservative
                                                                                                                       ; OKGANISM: P
US-08-743-637B-185
                                                                                                                   ORGANISM:
                                                                                                                                                                            Query Match
                                                                                                                                                                                              Best Local
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1179 GCTTAAGAAGGAGGGGGGGCGACACTCACCTTTCTTCCTGGTTACGCCCACAGTT 1238
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                                                         939 TATAGAGCGTGGCACCGTCAAGATTGGTGACACAGTCGATATCGTCGGAATCCGGGACAC 998
363 CGGTATCTTAGTTGTATCTGCTGCTGACGGTCCAATGCCACAAACTCGTGAACACATCTT 422
                                                                                                                                                                                             699 CGAGTACGACGCGACGACGTACCAATCGTCGCTGGCTCCGCCTCAAGGCGCTCGAGGC 758
                                                                                                                                                                                                                   1098 AGGIACAGAAATGGTTATGCCTGGCGACAACGTTGAAATGACAGTTGAATTAATCGCTCC
                                                                                                                  CGACGACGAGCAGCTCGTCGTCGAGCTCGAGCTCCGCGAGCTGCTCAGCAACTA
                                                                                                                                                                                                                                                                                                               ------AGGCGATGCTGAATACGAACAAAAATCTTAGA
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                                      579 CCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAGGACATGGT
                                                                                                                                                    483 AGACGACGAAGAATTATTAGAATTAGTTGAAATGGAAGTTCGTGACTTATTAAGCGAATA
                                                                                                                                                                                                                                                                        759 TCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTACATCTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kallender, Howard
APPLICANT: Van Horn, Stephanie
TITLE OF INVENTION: EF-Tu
FILE REFERENCE: GM10185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-218-197-1
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2540
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      1119 GGTGCTGGCAAAGCCTGGCTCTATCACCGCACACCAAGTTTGAGGCTGTTGTGTATGT 1178
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                            183 CACTGTTGCACAATCATACGATATGATTGACAACGCTCCAGAAGAAAAAAAGTAT
                                                                                     1179 GCTTAAGAAGGAAGAGGGTGGCCGACACTCACCTTTCTTCCCTGGTTACCGCCCACAGTT
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0; Mismatches 447; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   1419 CGGTGTCATCAACAAATCATTGAGTAA 1446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 24.0%;
Best Local Similarity 59.9%;
Matches 736; Conservative (
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                                                                                                                                                   Similarity 59.4%; Score 393.2; DB 4; Length 1185; Similarity 59.4%; Pred. No. 1.1e-82; Conservative 0; Mismatches 453; Indels 45;
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PastSEQ for Windows Version 4.0
SEG ID NO 1
LENGTH: 1185
                                                                                                  ; ORGANISM: Staphylococcus aureus
US-09-218-197-1
                                                                                                                                                                                   730;
                                                                                    TYPE: DNA
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Best Local (
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NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
Annoran
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1119 GGTGCTGGCAAAGCCTGGCTCTATCACACCGCACACGTTTGAGGCTGTTGTGTGTATGT 1178
                                                                   993 CTATTTCCGTACTACTGACGGAACTGGTGTTGT------TC----TCACTTACCAGA 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.9%; Score 368.8; DB 4;
59.5%; Pred. No. 7.8e-77;
tive 0; Mismatches 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                             1419 CGGTGTCATCAACAAATCATTGAGTAA 1446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 260, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 260:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PH
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STRANDEDNESS: double
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                       320 CGTCAGGTTGGTGTTAAACACCTTATCGTCTTCATGAACAAAGTTGACTTGGTTGACGAC 379
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                                     406 AACACCGCCACCGTCGAGTACGAGACCGAGACCCGCCACTACGCACGTCGACTGCCCC
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                                                                                                                   Sequence 642, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THERBOF
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1483 GITIACTCAAAGCGACATGCTCCGTAGTTGTTATTATGTGTGAGT 1528
                1175 AGACACTAAAAGAATCTTGCTTGGCAAGGTTCTTTTTTAGATATT 1220
                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
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ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
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REGISTRATION NUMBER: 32,430
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               755 PAGE MILL ROAD
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APPLICATION NUMBER: PP118
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-JAN-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PP291
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           TITLE OF INVENTION: P. GIN
NUMBER OF SEQUENCES: 1120
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650-494-0792
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Matches 432; Conservative
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HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CON OPERATING SYSTEM:
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TELEFAX: 650-49
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GENERAL INFORMATION:

APPLICANT: CLOUGH, BARBARA
APPLICANT: CLOUGH, BARBARA
APPLICANT: PREISER, PETER
APPLICANT: WILSON, ROBERT
TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: ANARIA PARASITE AND PROTEEN SYNTHESIS INHIBITORS
TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
FILE REFERENCE: N68837B GCW PJC DP
CURRENT PEPLICATION NUMBER: US,09/140,466
GURENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: US 60/056,246
EARLIER FILING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
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   CACCATCAACACCGCCACCGTCGAGTACGAGACCGAGACCCGCCACACACGTCGA
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                                                                 339 CAGCGCCCTAAGAAGTACGACGAGATCGACGCCCCCCCGAGGAGCGCCCCCGCGGTAT
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Patent No. 6268160
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; LOCATION: (1)..(1230)
US-09-140-466-1
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                                                         239 GCACCAAACCACACGTCAACATAGGCACCATGGCCCATGTCGACCACGGAAAGACCACTC 298
                                                                                                                 299 TCACCGCCGCGCTCACCATGGTGCTCGCCTCCGTCGGTGGCAGCGCGCCTAAGAAGTACG 358
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                                 Gaps
                                                                          23 GAAATAAACAACATATAAATTTAGGTACTATAGGCCATGTAGATCATGGAAAAACTACAT 82
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    Length 1230;
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 Score 188.8; DB 4;
Pred. No. 5.3e-35;
0; Mismatches 612;
Ouery Match
11.2%;
Best Local Similarity .48.5%;
Matches 585; Conservative
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3184 GATAACGTTGCTATGGACGTTGAATTAATTCACCCAATCGCTATCGAAGACGGAACTCGT 3125
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                 847 CCAGTCCCGCAGAGGCAGACTGACCTCCCGTTCTTGCTCGCTGTTGAAGATGTCTTCTCC 906
                                                                                                                             967 GACACAGTCGATATCGTCGGAATCCGGGAC---ACCCGGAACTGCACGGTCACTGGTGTT
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                                                                                                     ATCACCGGTCGTGCTACAGTTGCCACTGGCCGTATAGAGCGTGGCACCGTCAAGATTGGT
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FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for I
NUMBER OF SEQUENCES: 25
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APPLICANT: Ohno, 7
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1043 TAGATGTTACTG---GAGAAATTAAAAATATATATTTAAATGAAAAATGTACAAAAAGTAG 1099
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                                                             GCATGCCTGGTGACCGTATCAAAATGATTGTTCAGCTCATCCAGCCTGTTGCTTGTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
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58.2%; Pred. No. 2.8e-33;
ive 0; Mismatches 258;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTOWNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
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US-08-920-812-10/c
'S-equence 10, Application US/08920812
'Patent No. 5763188
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US-08-920-812-10
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
ITILE OF INVENTION: Probe for
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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Matches 386; Conservative
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EDNESS: double
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CORRESPONDENCE ADDRESS:
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APPLICANT: Ohno,
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CITY: Chicago
STATE: Illinois
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3064 TAA 3062

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1024 GAGATGTTCCAGAAGACCATGGATGATGCCATGGCCGGAGACAATGTTGGGCTGCTGCTC 1083
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Best Local Similarity 58.2%; Pred. No. 2.8e-33;
Matches 386; Conservative 0; Mismatches 258; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPRA: 312/474-0448
TELEPRA: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHRARACTERISTICS:
LENGTH: 3719 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
FRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                 υκGANISM: Enterococcus faecalis
; STRAIN: Clinical Isolate S2-3
US-08-920-827-10
                                                                                                                                                                                                                                                                                                                               Genomic DNA
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3708 GGCGACGACTTATGAAGAAAAATCTTAGAATTAATGGCTGCAGTTGACGAATATATC 3649
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                                                                                             APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Wehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
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58.2%; Pred. No. 2.8e-33;
tive 0; Mismatches 258;
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REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                         STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/921,177 FILING DATE: 29-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 10, Application US/08921177 Patent No. 5798211
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TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SRQUENCE CHARACTERISTICS:
TWOTH: 3719 base pairs
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Best Local Similarity 58.2°
Matches 386; Conservative
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                                                                              GENERAL INFORMATION:
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                 US-08-921-177-10/c
RESULT 11
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3468 GAAATGTTCCGTAAATTATTAGACTACGCTGAAGCAGGCGACAACATCGGTGCTTTATTA 3409
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1024 GAGATGTTCCAGAAGACCATGGATGATGCCATGGCCGGAGACAATGTTGGGCTGCTGCTC 1083
                                                                                       1084 CGTGGTATGCAGAAGGATGACATTGAAAGAGGCATGGTGCTGGCAAAGCCTGGCTCTATC
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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27-MAR-1995
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RY: United States of America
60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPAN: 312/474-6300
TELEFAX: 312/474-0448
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
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INFORMATION FOR SEQ ID NO: 10:
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LENGTH: 3719 base pairs
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STRANDEDNESS: double
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1204 CACTCACCTTTCTTCCCTGGTTACCGCCCACAGTTCTACATGCGGACAACTGATGTGACA 1263
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Uchara, Hirotsugu
APPLICANT: Bda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                  0; Mismatches 258;
                                                                                                                                                                                           Pred. No. 2.8e-33;
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                                                                       Enterococcus faecalis
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Patent No. 5853998
GENERAL INFORMATION:
                                                               ORGANISM: Enterococcus strain: Clinical Isolate S2-3
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                           58.2%;
                                                                                                                                                                                                                  Matches 386; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              967 GACACAGTCGATATCGTCGGAATCCGGGAC---ACCCGGAACTGCACGGTCACTGGTGTT 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1084 CGTGGTATGCAGAAGGATGACATTGAAAGAGGCATGGTGCTGGCAAAGCCTGGCTCTATC 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3408 cdrggrargangarararangangangangangangananganangangangang 3349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1204 CACTCACCTITCTTCCCTGGTTACCGCCCACAGTTCTACATGCGGACAACTGATGTGACA 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      847 CCAGTCCCGCAGAGGCAGACTGACCTCCCGTTCTTGCTCGCTGTTGAAGATGTCTTCTCC 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             907 ATCACCGGTCGTGGTACAGTTGCCACTGGCCGTATAGAGCGTGGCACCGTCAAGATTGGT 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 10.8%; Score 182.2; DB 2; Length 3719;
Best Local Similarity 58.2%; Pred. No. 2.8e-33;
Matches 386; Conservative 0; Mismatches 258; Indels 19; Gaps
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                             19036/32420
                                                                                                                                                SUPTWARE.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
                                : Illinois
XY: United States of America
60606-6402
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Enterococcus faecalis
STRAIN: Clinical Isolate S2-3
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                       NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                    TELERAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   : 3719 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                           CLASSIFICATION:
               Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; STRAIN: C
US-08-920-828-10
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3229 GGTGTTGT------AGAATTGCCAGAAGGTACTGAAATGGTAATGCCTGGT 3185
                                                                                   1324 GACCGTAICAAAATGAITGTICAGCTCAICCAGCCIGTTGCTTGTGAGCAGGGTAIGAG 1383
                                                                                                              1184 GATAACGIIGCIAIGGACGIIGAATIAAIICACCCAAICGCIAICGAAGACGGAACICGI 3125
                                                                                                                                                                    1384 TTTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGCCGGTGTCATCAACAAAATCATTGAG 1443
1264 GGGAGTGTGACTACGATTATGAATGACAAGGATGAGGAGGCGAAGATGTGCATGCCTGGT 1323
                                                                                                                                                                                            TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides, TITLE OF INVENTION: Polypeptides and Their Uses NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180.2; DB 4; Length 656; Pred. No. 4.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OSCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FLING DATE: 24-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION NATA:
APPLICATON NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/ACENT INCRAFATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 87, Application US/08936165A Patent No. 6348582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lonetto, Michael
Nicholas, Richar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%;
62.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Genomic DNA US-08-936-165A-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 656 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 709 sweet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hodgson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                    3064 TAA 3062
                                                                                                                                                                                                                                                           1444 TAA 1446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879 CITGCICGCIGITGAAGAIGICITCTCCATCACCGGICGIGGIACAGIIGCCACIGGCCG 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 CTTAATGCCCATTGAGGACGTGTTCTCTATCTCCGGACGAGGAACTGTAGTAACTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   939 TATAGAGCGIGGCACCGICAAGAIIGGIGACACAGICGAIAICGICGGAAICCGGGACAC 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 TAAAGAAACGATTGTTACTGGGGTTGAAATGTTCAGAAAAGAACTCCCAGAAGGTCGTGC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                               243 CTTAGTAGTATCTGCTGCTGACGGTCCAATGCCAAACTCGTGAACACATCTTTTATC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 CCTAAGAAGTACGACGAGGATCGACGCCCCCCGAGGAGCGCGCCCCGGGTATCACCATC 405
                                                                                                                                                                              63 GCACAATCATATGACATGATTGACAACGCTCCAGAAGAAAAAAGAACGTGGTATCACAATC 122
                                                                                                                                                                                                                               406 AACACCGCCACCGTCGAGTACGAGACCGAGACCCGCCACTACGCACACGTCGACTGCCCC 465
                                                                                                                                                                                                                                                          466 GG-CCACGCCGACTATGTCAAGAATATGATCACCGGCGCGTGCGCAGATGGACGGTGCCAT 524
                                                                                                                                                                                                                                                                                                                                                     183 GNATCCCGCTGACTACGTTAAAAACATGATCACTGGTGCTGCTCAAATGGACGGCGGTAT 242
                                                                                                                                                                                                                                                                                                                                                                                                                    525 CCTCGTCGTATCCGGTGCCGACGGCCCCATGCCGCAGACCAAAGAGCACATCCTCGC 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             585 CAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAGGACATGGTCGACGA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          645 CGAGGAGCTGCTCGAGCTCGTCGAGCTCGAGGTCCGCGAGCTGCTCAGCAACTACGAGTA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 TGAAGAATTATTAGAATTAGTAGAAATGGAAGTTCGTGACTTATTAAGCGAATATGACTT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                         286 GGAAAGACCACTCTCACCGCCGCGCTCACCATGGTGCTCGCCTCCGTCGGTGGCAGCGCG 345
                                                                                     3 GGTAAAACAACATTAACAGCAGCAATCGCTACTGTATTAGCAAAAAATGGTGACTCAGTT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 CCCAGGTGACGATGTACCTGTAATCGCTTCAGCATTAAAAGCTTTAGAAG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BABLE, Ajay
APPLICANT: Skelky, Yasir
APPLICANT: Skelky, Yasir
APPLICANT: Fling, Steve
APPLICANT: Fling, Steve
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 21011.4659556,877
CURRENT APPLICATION NUMBER: US/09/556,877
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       705 CGACGGCGACGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGCGCTCGAGG 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
0; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7%; Score 112.6; DB 4;
ilarity 60.7%; Pred. No. 1.9e-17;
Conservative 0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70, Application US/09556877 Patent No. 6432916
    295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 184; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Probst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US_09-556-877-70/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us-09-556-877-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
       Matches
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Fri May

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GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

May 1, 2003, 15:58:02; Search time 273 Seconds (without alignments) 7275.843 Million cell updates/sec Run on:

Perfect score: Sequence: Title:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

746064 seqs, 590810554 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_NA:*

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/ Ggn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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/ Ggn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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/ Cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: cgn2_6/ptodata/2/pubpna/US10_USUBCOMB.seq: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 7897, Ap	Sequence 7904, Ap	Sequence 86, Appl	Sequence 6265, Ap	Sequence 9866, Ap	Sequence 6334, Ap	Sequence 1, Appli	Sequence 3437, Ap	Sequence 7318, Ap	Sequence 3, Appli	Sequence 6962, Ap	Sequence 6972, Ap	Sequence 1309, Ap	Sequence 9073, Ap	Sequence 82, Appl	Sequence 8344, Ap	Sequence 4519, Ap	Sequence 6385, Ap	Sequence 3832, Ap
ΙĐ	US-09-815-242-7897	US-09-815-242-7904	US-09-912-020-86	US-09-815-242-6265	US-09-815-242-9866	US-09-815-242-6334	US-09-738-626-1	US-09-738-626-3437	US-09-815-242-7318	US-08-831-310-3	US-09-815-242-6962	US-09-815-242-6972	US-09-974-300-1309	US-09-815-242-9073	US-08-781-986A-82	US-09-815-242-8344	US-09-815-242-4519	US-09-815-242-6385	US-09-815-242-3832
ВВ В В	10	10	10	10	10	10	6	6	10	œ	10	10	10	10	7	10	10	10	10
% Query Match Length DB	1194	1194	1185	1185	1230	1185	3309400	1188	1200	1448	1185	1185	1057	1197	15598	1185	1182	1188	1185
& Query Match	31.4	31.0	30.3	30.3	30.1	30.0	26.8	26.6	25.9	25.9	25.0	25.0	24.6	23.6	23.4	23.4	23.2	22.5	22.4
Score	528.4	521.6	508.8	508.8	505.6	503.6	450.2	446.4	436	436	420.4	420.4	413.8	396.4	394	393.2	390.8	378.6	376.2
Result No.	н	2	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19

75 Sequence 575, App	6 Sequence 166, App	Sequence 164	1 Sequence 1, Appli	4 Sequence 154,	Sequence 526, App	8 Sequence 8	1 Sequence 15	'1 Sequence 171, App	9 Sequence 15	Sequence 1	8 Sequence 16	56 Sequence 4	2 Sequence	Sequence 155,	8 Sequence 158,	7 Sequence 147,	Sequence 162,	_	56 Sequence 156, App	Sequence 152,	8 Sequence 148,	8 Seguence 18,	Sequence 165,	7 Sequence 157,	sequence 125,	
US-09-925-300-575	US-09-989-643-166	US-09-989-643-164	US-09-070-927A-	US-09-989-643-15	US-09-841-132-5		_	US-09-989-643-17	0	US-09-790-988-1	US-09-989-643-16		US-10-007-693-5	_	US-09-989-643-15	US-09-989-643-14	US-09-989-643	US-09-989-643-1	US-09-989-643-1	US-09-989-643-15	US-09-989-643-14	US-10-007-693-1	US-09-989-643-16	US-09-989-643-15	US-09-989-643-12	
10	6	6	10	6	10	12	6	σ	6	10	6	10	12	6	6	6	6	φ	σ	σ	6	12	σ	σ	6	
1678	897	891	4315	891	1182	1182	894	606	891	640681	897	1185	1185	891	906	897	891	891	894	888	885	1377	881	891	814	
2.2	2.1	2.0	2.0	1.6	1.2	1.2	6.0	20.8	0.8	0.7	0.7	0.4	0.4	9.4	9.5	9.5	9.5	9.2	9.1	9.0	8.6	7.9	7.3	7.2	7.1	
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372.4	371.4	370.6	369.4	362.6	356.2	356.2	350.6	350	349.8	348.4	347.4	342.4	342.4	325.8	323.2	323	322.6	322.4	320.8	319.2	312.8	300.8	290.2	289	287.6	
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ALIGNMENTS

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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
AITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US/09/815,242
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PAPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7897
LENGTH: 1194
                                                 Sequence 7897, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa FEATURE:
                                                                                                                                                                 APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                            GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...(1194)
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; LOCATION: (1).
US-09-815-242-7897
RESULT 1
US-09-815-242-7897
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Fri May

	Query Match 31.4%; Score 528.4; DB 10; Length 1194; Best Local Similarity 66.1%; Pred. No. 5.3e-133; Matches 813; Conservative 0; Mismatches 381; Indels 36; Gaps	Qy 1237 TTCTACATGGGGA Qy 1237 TTCTACATGGGGA Db 1000 TTCTACTTCGTA
5 1	GGCACCATCGGCCA 	Oy 1297 GAGGAGGGAAGA
0 0	Oy 277 GTCGACCACGGAAAGACCACTCTCACCGCCGCTCACCATGGTGCTCGGTCGG	Qy 1357 Db 1105
U II	QY 337 GGCAGCGCCTAAGAAGTACGACGATCGACGCCCCCCGAGGAGCGCCCCGCGGT 396	Oy 1417 GCGGTGTCATCA
5 1	QY 397 ATCACCATCAACACGCCACĆGTCGAGTACGAGACCGAGACCGGCACTAGGCACGTC 456	. RE
5 1	QY 457 GACTGCCCGGCCACCGACTATGTCAAGAATATGATCACGGCGCTGCGCAGATGGAC 516	; Patent No. U; ; GENERAL INFO) ; APPLICANT:) ; APPLICANT:
υц	OY 517 GGTGCCATCCTCGTCGTGCTGCTGCTGGCCCATGCCGCAGACGACGACGACGTTG 576 1 1 1 1 1 1 1 1 1 1	
G D	A ST7 CTCCTCGCCAAGCAAGTCGTGTTCCCAAGATCGTTGTCTTCCTCAAGAAGAAGAAGG 636 16	; APPLICANT: Yamanoto ; APPLICANT: Xu, H. H. ; TITLE OF INVENTION: ; TITLE OF INVENTION:
5 0	QY 637 GTCGACGACGAGGAGCTGCTCGAGCTCGAGGTCGAGGTCGCGAGCTGCTCAGCAAC 696	
0 0	OY 697 TACGAGTACGACGACGACGTACCAATCGTCGCTCGCCTCCACGCCTCCAGGCGCTCGAG 756	
0 0	OY 757 GCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTACATCTTC 816 Db 541 GGCAAGGATGACAACGGCATCGGCGTAAGCGCCGTGCAG 579	
	QY 817 TCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTCCGCAGAGGCAGACTGACCTCCCG 876	
σΔ	QY 877 TTCTTGCTCGCTGTTGAAGATGTCTTCTCCATCACCGGTCGTGGTACAGTTGCCACTGGC 936	
σД	OY 937 CGTATAGAGCGTGGCACCGTCAAGATTGGTGACACAGTCGATATCGTCGGAATCCGGGAC 996	; LENGTH: ; TYPE: DN ; ORGANISM ; FEATURE:
αД	QY 997 ACCCGGAACTGCACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGATGATGATGCTG 1056	; NAME/KEY: CDS ; LOCATION: (1)(11' US-09-815-242-7904
σД	QY 1057 GCCGGAGACAATGTTGGGCTGCTGCTGGTATGCAGAAGGATGACATTGAAAGGGC 1116	Quer Best Matc
α Δ	OY 1117 ATGGTGCTGGCAAAGCCTGGCTCTATCACACCGCACACCAAGTTTGAGGCTGTTGTAT 1176	ବୁପ
0 0	QY 1177 GTGCTTAAGAAGGAAGGGTGGCCGACACTCACCTTTCTTCCTGGTTACCGCCCACAG 1236	0y 279 CGACCAGGAAGA 86 Db 63 TGACCATGGCAAGA
		OV 339 CAGCGCGCTAAG

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TGTGCATGCCTGGTGACCGTATCAAAATGATTGTTCAGCTCATCCAG 1356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.0%; Score 521.6; DB 10; Length 1194;
65.8%; Pred. No. 3.6e-131;
1ive 0; Mismatches 384; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              7: Identification of Essential Genes in

7: Identification of Essential Genes in

7: Prokaryotes

7: Trah.011A

N. NUMBER: US/09/815,242

NUMBER: 60/191,078

NUMBER: 60/191,078

1. 2000-03-21

NUMBER: 60/206,848

NUMBER: 60/207,727
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UMBER: 60/253,625
2000-11-27
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UMBER: 60/257,931
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MBER: 60/242,578
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1167 CGCCGTGGTTGCCAAGATCATCGAATAA 1194

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                                          CTGCCCCGGCCACGCCGACTATGTCAAGAATATGATCACCGGCGCTGCGCAGATGGACGG
                                                                                                          TGCCATCCTCGTCGTATCCGGTGCCGACGGCCCCATGCCGCAGACCAAAGAGCACATCCT
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TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN

TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN

FILE REPERENCE: ELITRA.001091,

CURRENT APPLICATION NUMBER: US/09/912,020

CURRENT PILING DATE: 2001-07-23

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 09/492,709

PRIOR FILING DATE: 1099-01-27

PRIOR FILING DATE: 1009-01-27

NUMBER OF SEQ ID NOS: 485

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 GCGGCGAGGGCAAGTTCGAGCGCACCAAACCACGTCAACATAGGCACCATCGGCCAT 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 508.8; DB 1
Pred. No. 1.1e-127
                ; Sequence 86, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
                                                                                                                                                                      Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.3%;
Best Local Similarity 65.3%;
Matches 803; Conservative
                                                                                                 Trawick, John
Forsyth, R. Allyn
Froelich, Jamie M.
                                                                 APPLICANT: Zyskind, Judith APPLICANT: Ohlsen, Kari L.
                                                                                                                                                      Carr, Grant J.
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US-09-912-020-86
JS-09-912-020-86
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APPLICANT:
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757 GCTCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTACATCTTC 816
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                                      ----AGGCGACGCAGAGTGGGAAGCGAAAATCCTG
                                                                                  817 TCGTTGGTTGATAAAGTGGATTCCTATATTCCAGTCCCGCAGAGGCAGACTGACCTCCCG
                                                                                                          877 ITCTTGCTCGCTGTTGAAGATGTCTTCTCCATCACCGGTCGTGGTACAGTTGCCACTGGC
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Tried of INVENTION: APPLICANT: Tried of INVENTION: Protestion of Essential Genes in
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65.3%; Pred. No. 1.1e-127
          PRIOR FILING DATE: 2000-10-2,
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                              Query Match 30.37
Best Local Similarity 65.33
Matches 803; Conservative
                                                                                                                                                                                                  TYPE: DNA ORGANISM: Escherichia coli
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LOCATION: (1).
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/205,848
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/205,848
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/255
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamotto, Robert T.
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ORGANISM: Salmonella typhi
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                                                                                                                           Length 1230;
                                                                                                                                                        Indels
                                                                                                                        30.1%; Score 505.6; DB 10; 65.1%; Pred. No. 8e-127;
                                                                                                                                                        0; Mismatches 385;
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                                                                             - A, T, C or
                                                                                                                                                       Matches 801; Conservative
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1230)
NAME/KEY: misc_feature
LOCATION: (1)...(1230)
OTHER INFORMATION: n = A
                                                                                                                                          Best Local Similarity
                                                                                            US-09-815-242-9866
                                                                                                                           Query Match
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63 TGACCATGGTAAAACAACGCTGACCGCTGCAATCACTACCGTACTGGCTAAAACCTACGG 122

279 CGACCACGGAAAGACCACTCTCACCGCCGCTCACCATGGTGCTCGCCTCCGTCGGTGG

90 90 90 90

3 GTCTAAAGAAAAGTTTGAACGTACAAAACCGCACGTTAACGTCGGTACTATCGGCCACGT 62

339 CAGCGCGCCTAAGAAGTACGACGAGATCGACGCCCCCCCGAGGAGGGCGCCCCGGGGTAT

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1296 TGAGGAGGCGAAGATGTGCATGCCTGGTGACCGTATCAAAATGATTGTTCAGCTCATCCA 1355
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                                                                1176 TGTGCTTAAGAAGGAAGAGGTGGCCGACACTCACCTTTCTTCCCTGGTTACCGCCCACA 1235
                                                                                          915 TCAGGTACTGGCTAAGCCGGGCACCATCAAGCCACACACCAAGTTCGAATCTGAAGTGTA 974
30.0%; Score 503.6; DB 10; Length 1185; 65.1%; Pred. No. 2.7e-126;
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tive 0; Mismatches 384; Indels
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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TITLE OF INVENTION: FIGNARYOUSES
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-29
PRIOR PLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
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PRIOR PELLING DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Matches 799; Conservative
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LENGTH: 1185
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APPLICANT:
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219 GGCGAGGGGAAGTTCGAGCGCACCAAACCACACGTCAACATAGGCACCATGGGCCATGT 278

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999 CCGGAACTGCACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGATGATGCCATGGC 1058
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                       183 CACCATCAACACTTCTCACGTTGAATACGACACCCGGACCCGTCACTACGCACACGTAGA
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                                                                              459 CTGCCCCGGCCACGCCGACTATGTCAAGAATATGATCACCGGCGCCTGCGCAGATGGACGG
                                                                                                     243 CTGCCCGGGCACGCCGACTATGTTAAAAACATGATCACCGGTGCTGCGCAGATGGACGG
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1359 TGTTGCTTGTGAGCAGGGTATGAGGTTTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGC 1418
                      CACATCCTCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAG 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR FILING DATE: 1999-12-16
PRIOR PELICATION NUMBER: JP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PARENTIN VET. 3.0
                                                                                    1419 CGGTGTCATCAACAAATCATTGAGTAA 1446
                                                                                                                         GGCCGTTGTAGCAAAGTTCTGAGCTAA 1185
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                                                                                                                                                                                                                                      Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                               MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
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                                                                                                     691 AGCAACTACGAGTACGACGACGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGCG
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Publication No. US20020197605A1
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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HAYASHI, MIKIRO
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IKEDA, MASATO
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TYPE: DNA
ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                           0; Mismatches 391;
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 3437
LENTH: 1188
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Matches 788; Conservative
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991 CGGGACA---CCCGGAACTGCACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGAT 1047
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-37
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
Wall, Daniel
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Ou. Mai	Query Match 25.9%; Score 4 Best Local Similarity 61.3%; Pred. N Matches 753; Conservative 0; Mism	re 436; DB 10; Length 1200; cd. No. 5.6e-108; Mismatches 445; Indels 30; Ga	ps 2;
λć qć	2) 219 GGCGAGGGCAAGTICGAGCGCACCAAACCACACGTCAACAIAGGCACCATGGCCATGT	CACGTCAACATAGGCACCATGGCCATGT 	278 62
ž g	279 CGACCACGGAAAGACCACTCTCACCGCGCTCACCATGGTGCTCGCTC	CTCACCATGGTGCTCGCCTCCGTCGGTGG	338
ķ g	2y 339 CAGGGGGCCTAAGAAGTACGAGGAGATGGACGCGCGCGCG	GCCGCCCCGGAGGAGCGCGCCGCGGGTAT	398 182
λχ op	2Y 399 CACCATCAACACGCCACGGTCGAGTACGAGACCGGAGACCGGCCACTACGCACGTCGA 	SACCGAGACCCGCCACTACGCACACGTCGA	458 242
y do	2y 459 CTGCCCGGCCACGCGACTATGTCAAGAATATGATCACCGGCGCTGCGCGAGATGGACGG	NATGATCACCGGCGCTGCGCAGATGGACGC	518 302
ž g	29 519 TGCCATCCTCGTCGTGCCGACGGCCCATGCCGAGACCAAGAGGCACATCTCT	OCCATGCGGGGGCGAAGGGGGGGTCCT 	578 362
ζ, G	DY 579 CCTCGCCAAGCAAGTCGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAAGGACATGGT	COTTGTCTTCCTCAACAAGAAGGACATGGT 	638 422
QY Dp	OY 639 GGACGAGGAGCTGCTCGAGCTCGAGCTCGAGGTCCGCGAGCTGCTCAGCAACTAGAAAAAAAA	CTCGAGGTCCGCGAGCTGCTCCAGCAACTA	698 482
č a	QY 699 CGAGTACGACGGCGACGATCGTCGCTGGCTCCGCCTCAAGGCGCTCGAGGC	GCTGGCTCCGCCCTCAAGGCGCTCGAGGC	758 541
è e	759 rcrcarggrcaa(CCTGCCTTGAAGCGCGGCGACGATGAGTGGGTCGACTACATCTTCTC	818 587
ος Op	QY 819 GTIGGTIGATAAAGIGGATICCIATATICCAGICCCGCAGAGGCAGACTGACCTCCCGTT	NGTCCCGCAGAGCAGACTGACCTCCCGTT	878 647
o o	QY 879 CTTGCTCGCTGTTGAAGATGTCTTCTCCATCACCGGTCGTGGTACAGTTGCCACTGGCCG	ACCGGTCGTGGTACAGTTGCCACTGGCCG	938
Oy Dp	QY 939 TATAGAGCGTGGCACCGTCAAGATTGGTGACACAGTCGATATCGTCGGAATCCGGGACAC 	PACAGTCGATATCGTCGGAATCCGGGACAC	998 767
Qy Dp	999 CCGGAACTGCACGGTCACTGGTGTTGAG 	ATGTTCCAGAAGACCATGGATGGTGCCATGGC 	1058 827
Oy Dp	OY 1059 CGGAGACAATGTTGGGCTGCTGCTCCGTGGTATGCAGAAGGATGACATTGAAAGAGGCAT 	ratgcagaaggatgacattgaaagaggcat 	1118 887
Q,	QY 1119 GGTGCTGGCAAAGCCTGGCTCTATCACACCGCACACAAGTTGAGGCTGTTGTGTATGT 	SCACACCAAGTTTGAGGCTGTTGTGTGTTGT 	1178 947

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Sequence 3, Application US/08831310
| Patent No. US20020026035A1
| SEGUENCE INFORMATION:
| APPLICANT: Riearthous, Harold et al. APPLICANT:
| TITLE OF INVENTION: Helicobacter GHPO 1360 and TITLE OF INVENTION: GHPO 750 Polypeptides and Corresponding Polynucleotides INUMBER OF SEQUENCES: 18
| CORRESPONDENCE ADDRESS: ADDRESSE: Clark & Elbing LLP | STREBT: 176 Federal Street | CITY: Boston | STREBT: 176 Federal Street | CITY: Boston | STREET: NAME | STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                            1179 GCTTAAGAAGGAAGAGGTGGCCGACACTCACCTTTCTTCCCTGGTTACCGCCCACAGTT 1238
                                        1359 TGTTGCTTGTGAGCAGGGTATGAGGTTTGCTATCCGTGAGGGTGGTAAGACCGTTGGTGC 1418
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06132/037001
TELECOMMUTICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPRAX: 617-428-7045
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COTHER INFORMATION:
US-08-831-310-3
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                           1230 TGTTGCGTTAGAGTTGGGAACTAAATTTGCGATTCGTGAAGGCGGTAGGACCGTTGGTGC 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                                                                           1419 CGGTGTCATCAACAAAATCATTGAGTAA 1446
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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PRIOR PLILING DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                      Sequence 6962, Application US/09815242 Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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Yamamoto, Robert T.
Xu, H. Howard
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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Best Local Similarity 60.8
Matches 747; Conservative
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US-09-815-242-6962
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                                                                                639 CGACGACGAGGAGCTCCTCGAGCTCGAGGTCCGCGAGCTGCTCAGCAACTA
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TYPE: DNA ORGANISM: Haemophilus influenzae

SEQ ID NO 6972

LENGTH:

; LOCATION: (1)... US-09-815-242-6972 NAME/KEY: CDS

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279 CGACCACGGAAAGACCACTCTCACCGCCGCTCACCATGGTGCTCGCCTCCGTCGGTGG 338
                                                                                                                                                                                                                339 CAGCGCGCCTAAGAAGTACGACGAGATCGACGCCGCCCCCGAGGAGGGGCGCCCGCGGTAT 398
                                                                                                                                                                                                                                                                                    399 CACCATCAACACCGCCACCGTCGAGTACGAGACCGAGACCCGCCACTACGCACACGTCGA 458
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                                          45;
Ouery Match 25.0%; Score 420.4; DB 10; Length Best Local Similarity 60.8%; Pred. No. 9.3e-104; Matches 747; Conservative 0; Mismatches 436; Indels
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Sequence 6972, Application US/09815242 Patent No. US20020061569A1

RESULT 12 US-09-815-242-6972

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Length 1185;

APPLICANT: TITALK, JOHN D.
APPLICANT: TITALK, JOHN D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/015,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR PELLON NUMBER: 60/259,308
PRIOR FILING DATE: 2001-12-12

Ohlsen, Kari L. Zyskind, Judith W. Wall, Daniel Trawick, John D. Haselbeck, Robert

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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1119 GGTGCTGGCAAAGCCTGGCTCTATCACACCGCACACCAAGTTTGAGGCTGTTGTGTATGT 1178
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423 AGATGACGAAGAGTTATTAGAATTAGTCGAAATGGAAGTTCGTGAACTTCTATCTCAATA 482
                                           699 CGAGTACGACGGCGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGCGCTCGAGGC 758
                                                                  483 TGACTTCCCAGGTGACGATACACCAATCGTACGTGGTTCAGCATTACAAGCGTTAAA---
                                                                                                                                                                                                                                                                                                                                     759 TCTCATGGTCAACCCTGCCTTGAAGCGCGCGACGATGAGTGGGTCGACTACATCTTCTC
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APPLICANT: Clausen, 1b Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
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FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR PAPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FASTSEQ for Windows Version 4.0
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1113 AGGCATGGTGCTGGCAAAGCCTGGCTCTATCACACCGCACCAAGTTTGAGGCTGTTGT 1172
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                                                                                                                                                                        219 GGCGAGGGGCAAGTICGAGCGCACCAAACCACGTCAACATAGGCACCATCGGCCATGT 278
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                                                                                                   Length 1057;
                                                                                                 Score 413.8; DB 10; Length
Pred. No. 5.4e-102;
0; Mismatches 337; Indels
                                   TYPE: DNA ORGANISM: Bacillus licheniformis
                                                                                                       24.6%;
64.6%;
                                                                                                                                          Matches 682; Conservative
                                                                                                                           Similarity
                                                          ; ORGANISM: BAULI
US-09-974-300-1309
SEQ ID NO 1309
                LENGTH: 1057
                                                                                                          Query Match
Best Local 8
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1173 GTATGTGCTTAAGAAGGAAGAGGGTGGCCGACACTCACCTTTCTTCCCTGGTTACCGCCC 1232
                                          219 GGCGAGGGCCAAGTTCGAGCGCACCAAACCACGTCAACATAGGCACCATCGGCCATGT 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tautaminolo, RODELL 1.

APPLICANT: XU, H Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR APPLICATION NUMBER: 00/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-23

PRIOR PLICATION NUMBER: 60/203,727

PRIOR PLICATION NUMBER: 60/203,727

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                               993 TCAGTTCTACTTCCGTACAACTGACGTAACTGGTA 1027
                                                                                                                                        1233 ACAGTTCTACATGCGGACAACTGATGTGACAGGGA 1267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawlck, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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US-09-815-242-9073
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990 C---CGGGACACCCGGAACTGCACGGTCACTGGTGTTGAGATGTTCCAGAAGACCATGGA 1046
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                                                                                                                                                              693 ITCAGGACGTATCGTGTATCGTTAAAGTCAACGACGAAATCGAAATCGTTGGTAT 752
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                    243 TCACATCGACGCTCCAGGACACGCGGACTACGTTAAAAACATGATCACTGGTGCTGCA
                                                                   450 ACACGTCGACTGCCCCGGCCACGCCGACTATGTCAAGAATATGATCACCGGCGCTGCGCA
                                                                                                        303 AATGGACGGAGCTATCCTTGTAGTAGCTTCAACTGACGGACCAATGCCACAAACTCGTGA
                                                                                                                                         GCACATCCTCCTCGCCAAGCAAGTCGGTGTTCCCAAGATCGTTGTCTTCCTCAACAAGAA
                                                                                                                                                                                                                                                                                   690 CAGCAACTACGAGTACGACGGCGACGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGC
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Sequence 82, Application US/08781986A Publication No. US20030054436A1

US-08-781-986A-82

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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 307446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 15598 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DAT
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                  MEDIUM TYPE: Disket: COMPUTER: HP Vectra OPERATING SYSTEM: M.
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                             ADDRESSEE: Human Ge
STREET: 9410 Key We
                                                                                                                                                                                                                    COMPUTER READABLE FORM
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                                                                                                                                                       STATE: Maryland
                                                                                                                                       Rockville
GENERAL INFORMATION:
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                                                                                                                                                                              USA
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                                                                                                                                                                                             20850
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                                                                                                                                                                              COUNTRY:
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12752 GATCCCTCAATCGAGGGGTCTTTTTTTAATGTGTAAATTTTGTAATGGCTATTTA 12811
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                            -----AGGCGATGCTCAATACGAAAAAATCTTAGA 12106
                                                                                                                                                                                                                            12107 ATTAATGGAAGCTGTAGATACTTACATTCCAACTCCAGAACGTGATTCTGACAAACCATT 12166
                                                                                                                                                                                                                                                                                                 12347 IGGIGACAACATIGGIGCATIATIACGIGGIGTIGCTCGIGAAGACGIACAACGIGGICA 12406
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699 CGAGTACGACGCGACGACGTACCAATCGTCGCTGGCTCCGCCCTCAAGGCGCTCGAGGC 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12467 ATTATCAAAAGACGAAGGTGGACGTCACACTCCATTCTTCTCAAACTATCGTCCACAATT
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                                                                                           759 TCTCATGGTCAACCCTGCCTTGAAGCGCGGCGACGATGAGGTGGGTCGACTACATCTTCTC
                                                                                                                                                                                   819 GITGGTTGATAAAGTGGATTCCTATATTCCAGTCCCGCAGAGGCAGACTGACCTCCCGTT
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Search completed: May 1, 2003, 22:09:46 Job time: 1226 secs